

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2005, 15:23:29 ; Search time 164 Seconds  
(without alignments)  
221.680 Million cell updates/sec

Title: US-09-688-566-81  
Perfect score: 494  
Sequence: 1 VSDVRDLVVAAFTSRLL.....VTKSDTYKYDDPISINYRT 94

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	494	100.0	94	5	Abb78898 Tumour ne
2	494	100.0	94	5	Abb78921 Tumour ne
3	489	99.0	94	5	Abb78939 Tumour ne
4	489	99.0	94	5	Abb78919 Tumour ne
5	489	99.0	94	5	Abb78920 Tumour ne
6	488	98.8	94	5	Abb78911 Tumour ne
7	486	98.4	94	5	Abb78915 Tumour ne
8	484	98.0	94	5	Abb78940 Tumour ne
9	484	98.0	94	5	Abb78912 Tumour ne
10	483	97.8	94	5	Abb78916 Tumour ne
11	483	97.8	94	5	Abb78918 Tumour ne
12	481	97.4	94	5	Abb78899 Tumour ne
13	478	96.8	94	5	Abb78917 Tumour ne
14	463	93.7	94	5	Abb78922 Tumour ne
15	446	90.3	94	5	Abb78923 Tumour ne
16	443	89.7	94	5	Abb78949 Tumour ne
17	439	88.9	94	5	Abb78873 Tumour ne
18	437.5	88.6	93	5	Abb78869 Tumour ne
19	437	88.5	93	5	Abb78868 Tumour ne
20	431	87.2	94	5	Abb78872 Tumour ne
21	419	84.8	94	5	Abb78942 Tumour ne
22	417	84.4	94	5	Abb78870 Tumour ne
23	416	84.2	94	5	Abb78900 Tumour ne
24	415	84.0	94	5	Abb78871 Tumour ne
25	406	82.2	94	5	Abb78895 Tumour ne

26	402	81.4	94	5	ABB78941	Abb78941	Tumour ne
27	397	80.4	94	5	ABB78901	Abb78901	Tumour ne
28	395	80.0	76	5	ABB78897	Abb78897	Tumour ne
29	393	79.6	94	5	ABB78880	Abb78880	Tumour ne
30	392	79.4	94	5	ABB78879	Abb78879	Tumour ne
31	392	79.4	94	5	ABB78928	Abb78928	Tumour ne
32	390	78.9	94	5	ABB78954	Abb78954	Tumour ne
33	390	78.9	94	5	ABB78910	Abb78910	Tumour ne
34	389	78.7	94	5	ABB78881	Abb78881	Tumour ne
35	389	78.7	94	5	ABB78909	Abb78909	Tumour ne
36	388	78.5	94	5	ABB78950	Abb78950	Tumour ne
37	388	78.5	94	5	ABB78876	Abb78876	Tumour ne
38	387.5	78.4	93	5	ABB78896	Abb78896	Tumour ne
39	385	77.9	94	5	ABB78864	Abb78864	Tumour ne
40	384	77.7	94	5	ABB78867	Abb78867	Tumour ne
41	384	77.7	94	5	ABB78904	Abb78904	Tumour ne
42	382.5	77.4	93	5	ABB78878	Abb78878	Tumour ne
43	382	77.3	94	5	ABB78877	Abb78877	Tumour ne
44	380	76.9	94	5	ABB78866	Abb78866	Tumour ne
45	374	75.7	94	5	ABB78929	Abb78929	Tumour ne

ALIGNMENTS

RESULT 1  
ABB78898  
ID ABB78898 standard; peptide; 94 AA.  
XX AC ABB78898;  
XX DT 30-JUL-2002 (first entry)  
XX DE Tumour necrosis factor-alpha binding amino acid sequence T10.06.  
XX KW Protein scaffold; antibody; binding protein; immunoglobulin;  
XX KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX FN WO200232925-A2.  
XX PD 25-APR-2002.  
XX PF 16-OCT-2001; 2001WO-US032233.  
XX PR 16-OCT-2000; 2000US-00688566.  
XX PA (PHYL-) PHYLLOS INC.  
XX PI Lipovsek D, Wagner RW, Kuimelis RG;  
XX DR WPI; 2002-444238/47.  
XX PT New non-antibody proteins having an immunoglobulin fold, useful in  
XX PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
XX PT designing proteins with specific properties, e.g. for binding any antigen  
XX PT of interest.  
XX PS Claim 47; Fig 25; 94pp; English.  
XX CC The present invention describes a non-antibody protein, comprising a  
XX CC domain having an immunoglobulin-like fold, derived from a reference  
XX CC protein having a mutated amino acid sequence, where the non-antibody  
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
XX CC not bound as tightly by the reference protein. The non-antibody protein  
XX CC is useful as scaffolds for selecting or designing a protein framework  
XX CC with specific and favourable properties, e.g. for binding any antigen of  
XX CC interest, or for destroying or inactivating antibody molecules. The non-  
XX CC antibody protein is also useful in all areas where antibodies are used,  
XX CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
XX CC binding proteins useful in the above-mentioned fields. The present

CC proteins have thermodynamic properties superior to those of natural  
 CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
 CC antibody mimics exhibit improved biophysical properties, such as  
 CC stability under reducing conditions and solubility at high  
 CC concentrations. In addition, these molecules are readily expressed and  
 CC folded in prokaryotic systems (e.g. *Escherichia coli*), in eukaryotic  
 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
 CC reticulocyte lysate system). Furthermore, these proteins are extremely  
 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention  
 XX  
 XX Sequence 94 AA;

Query Match 100.0%; Score 494; DB 5; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1e-49; Indels 0; Gaps 0;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
 Db 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
 QY 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
 Db 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94

RESULT 2  
 ABB78921  
 ID ABB78921 standard; peptide; 94 AA.  
 XX  
 AC ABB78921;  
 XX  
 DT 30-JUL-2002 (first entry)  
 XX  
 DE Tumour necrosis factor-alpha binding amino acid sequence T14.26.  
 XX  
 KW Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200232925-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 16-OCT-2001; 2001WO-US032233.  
 XX  
 PR 16-OCT-2000; 2000US-00688566.  
 XX  
 PA (PHYL-) PHYLOS INC.  
 XX  
 PI Lipovsek D, Wagner RW, Kuimelis RG;  
 XX  
 DR WPI; 2002-444238/47.  
 XX  
 PT New non-antibody proteins having an immunoglobulin fold, useful in  
 PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
 PT designing proteins with specific properties, e.g. for binding any antigen  
 PT of interest.  
 XX  
 PS Claim 47; Fig 25; 94pp; English.

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 CC domain having an immunoglobulin-like fold, derived from a reference  
 CC protein having a mutated amino acid sequence, where the non-antibody  
 CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
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 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
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 CC the exemplification of the present invention  
 XX  
 XX Sequence 94 AA;

Query Match 100.0%; Score 494; DB 5; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1e-49; Indels 0; Gaps 0;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
 Db 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
 QY 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
 Db 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94

RESULT 3  
 ABB78939  
 ID ABB78939 standard; peptide; 94 AA.  
 XX  
 AC ABB78939;  
 XX  
 DT 30-JUL-2002 (first entry)  
 XX  
 DE Tumour necrosis factor-alpha binding amino acid sequence M12.01.  
 XX  
 KW Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200232925-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 16-OCT-2001; 2001WO-US032233.  
 XX  
 PR 16-OCT-2000; 2000US-00688566.  
 XX  
 PA (PHYL-) PHYLOS INC.  
 XX  
 PI Lipovsek D, Wagner RW, Kuimelis RG;  
 XX  
 DR WPI; 2002-444238/47.  
 XX  
 PT New non-antibody proteins having an immunoglobulin fold, useful in  
 PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
 PT designing proteins with specific properties, e.g. for binding any antigen  
 PT of interest.  
 XX  
 PS Claim 47; Fig 25; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a  
 CC domain having an immunoglobulin-like fold, derived from a reference  
 CC protein having a mutated amino acid sequence, where the non-antibody  
 CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
 CC not bound as tightly by the reference protein. The non-antibody protein  
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 CC proteins have thermodynamic properties superior to those of natural  
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 CC stability under reducing conditions and solubility at high  
 CC concentrations. In addition, these molecules are readily expressed and  
 CC folded in prokaryotic systems (e.g. *Escherichia coli*), in eukaryotic  
 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
 CC reticulocyte lysate system). Furthermore, these proteins are extremely  
 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 99.0%; Score 489; DB 5; Length 94;  
 Best Local Similarity 97.9%; Pred. No. 3.9e-49;  
 Matches 92; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLOSRYRITYGTGNSPVQETVPPWASIIATIS 60  
 Db 1 VSDVPRDLEVVAAATPTSLISWNRSGLOSRYRITYGTGNSPVQETVPPWASIIATIS 60  
 Qy 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
 Db 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94

RESULT 4

ABB78919  
 ID ABB78919 standard; peptide; 94 AA.

XX ABB78919;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence T14.14.

XX Protein scaffold; antibody; binding protein; immunoglobulin;  
 XX tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.  
 XX Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2002-444238/47.

XX New non-antibody proteins having an immunoglobulin fold, useful in  
 XX research, therapeutic or diagnostic fields, particularly as scaffolds for  
 XX designing proteins with specific properties, e.g. for binding any antigen  
 XX of interest.

XX Claim 47; Fig 25; 94pp; English.

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CC protein having a mutated amino acid sequence, where the non-antibody  
 CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
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 CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 99.0%; Score 489; DB 5; Length 94;  
 Best Local Similarity 98.9%; Pred. No. 3.9e-49;  
 Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLOSRYRITYGTGNSPVQETVPPWASIIATIS 60  
 Db 1 VSDVPRDLEVVAAATPTSLISWNRSGLOSRYRITYGTGNSPVQETVPPWASIIATIS 60  
 .Qy 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
 Db 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94

RESULT 5

ABB78920  
 ID ABB78920 standard; peptide; 94 AA.

XX ABB78920;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence T14.23.

XX Protein scaffold; antibody; binding protein; immunoglobulin;  
 XX tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.  
 XX Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2002-444238/47.

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XX Claim 47; Fig 25; 94pp; English.

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XX CC protein having a mutated amino acid sequence, where the non-antibody
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XX CC antibody protein is also useful in all areas where antibodies are used,
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XX CC selection, e.g. in vitro selection using RNA-protein fusion technology,
XX CC phage display or yeast display systems. The present sequence is used in
XX CC the exemplification of the present invention
XX SQ Sequence 94 AA;
      Query Match          99.0%; Score 489; DB 5; Length 94;
      Best Local Similarity 98.9%; Pred. No. 3.9e-49;
      Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
      QY 1 VSDVPRDLEVVAAATPTRLISWNRSGLQSRYYRITYGETGNSPVQETVPPWASIATIS 60
      Db 1 VSDVPRDLEVVAAATPTRLISWNRSGLQSRYYRITYGETGNSPVQETVPPWASIATIS 60
      QY 61 GLKPGVDYTTVYAVATKSDTYKYDDPISINRYT 94
      Db 61 GLKPGVDYTTVYAVADKSDTYKYDDPISINRYT 94
      RESULT 6
      ABB78911
      ID ABB78911 standard; peptide; 94 AA.
      XX
      AC ABB78911;
      XX
      DT 30-JUL-2002 (first entry)
      XX
      DE Tumour necrosis factor-alpha binding amino acid sequence S08.02.
      XX
      KW Protein scaffold; antibody; binding protein; immunoglobulin;
      KW tumour necrosis factor alpha; TNF-alpha; protein framework.
      XX
      OS Homo sapiens.
      OS Synthetic.
      XX
      PN WO200232925-A2.
      XX
      PD 25-APR-2002.
      XX
      XX 16-OCT-2001; 2001WO-US032233.
      XX
      XX 16-OCT-2000; 2000US-00688566.
      XX
      XX (PHYL-) PHYLLOS INC.
      PA
      PA Lipovsek D, Wagner RW, Kuimelis RG;
      XX
      XX WPI; 2002-444238/47.
      DR
      XX
      XX New non-antibody proteins having an immunoglobulin fold, useful in
      PT research, therapeutic or diagnostic fields, particularly as scaffolds for
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CC binding proteins useful in the above-mentioned fields. The present  
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CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
CC reticulocyte lysate system). Furthermore, these proteins are extremely  
CC amenable to affinity maturation techniques involving multiple cycles of  
CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
CC phage display or yeast display systems. The present sequence is used in  
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 98.4%; Score 486; DB 5; Length 94;

Best Local Similarity 97.9%; Pred. No. 8.7e-49;

Matches 92; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQETVPPWASIAIS 60

Db 1 LSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQETVPPWASIAIS 60

Qy 61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINRT 94

Db 61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINRT 94

RESULT 8

ABB78940

ID ABB78940 standard; peptide; 94 AA.

XX ABB78940;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence M12.01.

XX Protein scaffold; antibody; binding protein; immunoglobulin;  
XX tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

OS Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

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XX WPI; 2002-444238/47.

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CC concentrations. In addition, these molecules are readily expressed and  
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CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
CC reticulocyte lysate system). Furthermore, these proteins are extremely  
CC amenable to affinity maturation techniques involving multiple cycles of  
CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
CC phage display or yeast display systems. The present sequence is used in  
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 98.0%; Score 484; DB 5; Length 94;

Best Local Similarity 96.8%; Pred. No. 1.5e-48;

Matches 91; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQETVPPWASIAIS 60

Db 1 VSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQETVPPWASIAIS 60

Qy 61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINRT 94

Db 61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINRT 94

RESULT 9

ABB78912

ID ABB78912 standard; peptide; 94 AA.

XX ABB78912;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence S08.03.

XX Protein scaffold; antibody; binding protein; immunoglobulin;  
XX tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

OS Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.



PD 25-APR-2002.  
 XX 16-OCT-2001; 2001WO-US032233.  
 XX 16-OCT-2000; 2000US-00688566.  
 XX (PHYL-) PHYLLOS INC.  
 XX Lipovsek D, Wagner RW, Kuimelis RG;  
 XX WPI; 2002-444238/47.  
 XX  
 XX New non-antibody proteins having an immunoglobulin fold, useful in  
 PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
 PT designing proteins with specific properties, e.g. for binding any antigen  
 PT of interest.  
 XX  
 PS Claim 47; Fig 25; 94pp; English.  
 XX  
 XX The present invention describes a non-antibody protein, comprising a  
 CC domain having an immunoglobulin-like fold, derived from a reference  
 CC protein having a mutated amino acid sequence, where the non-antibody  
 CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
 CC not bound as tightly by the reference protein. The non-antibody protein  
 CC is useful as scaffolds for selecting or designing a protein framework  
 CC with specific and favourable properties, e.g. for binding any antigen of  
 CC interest, or for destroying or inactivating antibody molecules. The non-  
 CC antibody protein is also useful in all areas where antibodies are used,  
 CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
 CC binding proteins useful in the above-mentioned fields. The present  
 CC proteins have thermodynamic properties superior to those of natural  
 CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
 CC antibody mimics exhibit improved biophysical properties, such as  
 CC stability under reducing conditions and solubility at high  
 CC concentrations. In addition, these molecules are readily expressed and  
 CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic  
 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
 CC reticulocyte lysate system). Furthermore, these proteins are extremely  
 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention  
 XX  
 SQ Sequence 94 AA;  
 Query Match 97.8%; Score 483; DB 5; Length 94;  
 Best Local Similarity 97.9%; Pred. No. 1.9e-48;  
 Matches 92; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQSYRYRITYGETGNSPVQFTVPWPWASIATIS 60  
 Db 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQSYRYRITYGETGNSPVQFTVPWPWASMATIS 60  
 Qy 61 GLKPGVDYITVVAATDKSDTYKYDDPISINVRT 94  
 Db 61 GLKPGVDYITVVAATDKSDTYKYDDPISINVRT 94  
 RESULT 12  
 ABB78899  
 ID ABB78899 standard; peptide; 94 AA.  
 XX ABB78899;  
 XX  
 XX 30-JUL-2002 (first entry)  
 XX Tumour necrosis factor-alpha binding amino acid sequence T10.17.  
 XX Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
 XX Homo sapiens.  
 OS Synthetic.

XX WO200232925-A2.  
 XX 25-APR-2002.  
 XX 16-OCT-2001; 2001WO-US032233.  
 XX 16-OCT-2000; 2000US-00688566.  
 XX (PHYL-) PHYLLOS INC.  
 XX Lipovsek D, Wagner RW, Kuimelis RG;  
 XX WPI; 2002-444238/47.  
 XX  
 XX New non-antibody proteins having an immunoglobulin fold, useful in  
 PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
 PT designing proteins with specific properties, e.g. for binding any antigen  
 PT of interest.  
 XX  
 PS Claim 47; Fig 25; 94pp; English.  
 XX  
 XX The present invention describes a non-antibody protein, comprising a  
 CC domain having an immunoglobulin-like fold, derived from a reference  
 CC protein having a mutated amino acid sequence, where the non-antibody  
 CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
 CC not bound as tightly by the reference protein. The non-antibody protein  
 CC is useful as scaffolds for selecting or designing a protein framework  
 CC with specific and favourable properties, e.g. for binding any antigen of  
 CC interest, or for destroying or inactivating antibody molecules. The non-  
 CC antibody protein is also useful in all areas where antibodies are used,  
 CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
 CC binding proteins useful in the above-mentioned fields. The present  
 CC proteins have thermodynamic properties superior to those of natural  
 CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
 CC antibody mimics exhibit improved biophysical properties, such as  
 CC stability under reducing conditions and solubility at high  
 CC concentrations. In addition, these molecules are readily expressed and  
 CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic  
 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
 CC reticulocyte lysate system). Furthermore, these proteins are extremely  
 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention  
 XX  
 SQ Sequence 94 AA;  
 Query Match 97.4%; Score 481; DB 5; Length 94;  
 Best Local Similarity 98.9%; Pred. No. 3.3e-48;  
 Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQSYRYRITYGETGNSPVQFTVPWPWASIATIS 60  
 Db 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQSYRYRITYGETGNSPVQFTVPWPWASIATIS 60  
 Qy 61 GLKPGVDYITVVAATDKSDTYKYDDPISINVRT 94  
 Db 61 GLKPGVDYITVVAATDKSDTYKYDDPISINVRT 94  
 RESULT 13  
 ABB78917  
 ID ABB78917 standard; peptide; 94 AA.  
 XX ABB78917;  
 XX  
 XX 30-JUL-2002 (first entry)  
 XX Tumour necrosis factor-alpha binding amino acid sequence T14.17.  
 XX Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.



```

XX OS Homo sapiens.
XX KW Synthetic.
XX PN WO200232925-A2.
XX PD 25-APR-2002.
XX PF 16-OCT-2001; 2001WO-US032233.
XX PR 16-OCT-2000; 2000US-00688566.
XX PA (PHYL-) PHYLLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX DR WPI; 2002-444238/47.
XX PT New non-antibody proteins having an immunoglobulin fold, useful in
XX PT research, therapeutic or diagnostic fields, particularly as scaffolds for
XX PT designing proteins with specific properties, e.g. for binding any antigen
XX PS of interest.
XX PS Claim 47; Fig 25; 94pp; English.
XX CC The present invention describes a non-antibody protein, comprising a
XX CC domain having an immunoglobulin-like fold, derived from a reference
XX CC protein having a mutated amino acid sequence, where the non-antibody
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is
XX CC not bound as tightly by the reference protein. The non-antibody protein
XX CC is useful as scaffolds for selecting or designing a protein framework
XX CC with specific and favourable properties, e.g. for binding any antigen of
XX CC interest, or for destroying or inactivating antibody molecules. The non-
XX CC antibody protein is also useful in all areas where antibodies are used,
XX CC e.g. research, therapeutic or diagnostic fields, and for screening novel
XX CC binding proteins useful in the above-mentioned fields. The present
XX CC proteins have thermodynamic properties superior to those of natural
XX CC antibodies, and can be evolved rapidly in vitro. The present proteins or
XX CC stability under reducing conditions and solubility at high
XX CC concentrations. In addition, these molecules are readily expressed and
XX CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX CC reticulocyte lysate system). Furthermore, these proteins are extremely
XX CC amenable to affinity maturation techniques involving multiple cycles of
XX CC selection, e.g. in vitro selection using RNA-protein fusion technology,
XX CC phage display or yeast display systems. The present sequence is used in
XX CC the exemplification of the present invention
XX SQ Sequence 94 AA;
XX Query Match 96.8%; Score 478; DB 5; Length 94;
XX Best Local Similarity 97.9%; Pred. No. 7.5e-48;
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XX Db 61 GLKHGVDYITTYVAVTDKSDTYKYDDPISINVRT 94
XX RESULT 14
XX ABB78922
XX ID ABB78922 standard; peptide; 94 AA.
XX AC ABB78922;
XX XX 30-JUL-2002 (first entry)
XX DT Tumour necrosis factor-alpha binding amino acid sequence T14.24.
XX DE

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XX OS Protein scaffold; antibody; binding protein; immunoglobulin;
XX KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX PN Homo sapiens.
XX OS Synthetic.
XX PN WO200232925-A2.
XX PD 25-APR-2002.
XX PF 16-OCT-2001; 2001WO-US032233.
XX PR 16-OCT-2000; 2000US-00688566.
XX PA (PHYL-) PHYLLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX DR WPI; 2002-444238/47.
XX PT New non-antibody proteins having an immunoglobulin fold, useful in
XX PT research, therapeutic or diagnostic fields, particularly as scaffolds for
XX PT designing proteins with specific properties, e.g. for binding any antigen
XX PT of interest.
XX PS Claim 47; Fig 25; 94pp; English.
XX CC The present invention describes a non-antibody protein, comprising a
XX CC domain having an immunoglobulin-like fold, derived from a reference
XX CC protein having a mutated amino acid sequence, where the non-antibody
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is
XX CC not bound as tightly by the reference protein. The non-antibody protein
XX CC is useful as scaffolds for selecting or designing a protein framework
XX CC with specific and favourable properties, e.g. for binding any antigen of
XX CC interest, or for destroying or inactivating antibody molecules. The non-
XX CC antibody protein is also useful in all areas where antibodies are used,
XX CC e.g. research, therapeutic or diagnostic fields, and for screening novel
XX CC binding proteins useful in the above-mentioned fields. The present
XX CC proteins have thermodynamic properties superior to those of natural
XX CC antibodies, and can be evolved rapidly in vitro. The present proteins or
XX CC stability under reducing conditions and solubility at high
XX CC concentrations. In addition, these molecules are readily expressed and
XX CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX CC reticulocyte lysate system). Furthermore, these proteins are extremely
XX CC amenable to affinity maturation techniques involving multiple cycles of
XX CC selection, e.g. in vitro selection using RNA-protein fusion technology,
XX CC phage display or yeast display systems. The present sequence is used in
XX CC the exemplification of the present invention
XX SQ Sequence 94 AA;
XX Query Match 93.7%; Score 463; DB 5; Length 94;
XX Best Local Similarity 93.6%; Pred. No. 4.3e-46;
XX Matches 88; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX QY 1 VSDVPRDLEVVAATPTSLRISWNRSGLQSRYYRITYTGETGNSPVQEFVPPWASITATIS 60
XX Db 1 VSDVPRDLEVVAATPTSLRISWNRSGLQSRYYRITYTGETGNSPVQEFVPPWASITATIS 60
XX QY 61 GLKPGVDYITTYVAVTDKSDTYKYDDPISINVRT 94
XX Db 61 GLKPGVDYITTYVAVTDKSDTYKYDDPISINVRT 94
XX RESULT 15
XX ABB78923
XX ID ABB78923 standard; peptide; 94 AA.
XX AC ABB78923;
XX XX
XX XX

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DT 30-JUL-2002 (first entry)  
XX Tumour necrosis factor-alpha binding amino acid sequence T14.20.  
DE  
XX  
XX Protein scaffold; antibody; binding protein; immunoglobulin;  
KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
KW  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200232925-A2.  
PN  
XX  
XX 25-APR-2002.  
PD  
XX  
XX 16-OCT-2001; 2001WO-US032233.  
PF  
XX  
XX 16-OCT-2000; 2000US-00688566.  
PR  
XX (PHYL-) PHYLLOS INC.  
PA  
XX Lipovsek D, Wagner RW, Kuimelis RG;  
PI WPI; 2002-444238/47.  
XX  
XX  
XX New non-antibody proteins having an immunoglobulin fold, useful in  
PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
PT designing proteins with specific properties, e.g. for binding any antigen  
PT of interest.  
PT  
XX  
PS Claim 47; Fig 25; 94pp; English.  
XX  
XX The present invention describes a non-antibody protein, comprising a  
CC domain having an immunoglobulin-like fold, derived from a reference  
CC protein having a mutated amino acid sequence, where the non-antibody  
CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
CC not bound as tightly by the reference protein. The non-antibody protein  
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CC with specific and favourable properties, e.g. for binding any antigen of  
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CC binding proteins useful in the above-mentioned fields. The present  
CC proteins have thermodynamic properties superior to those of natural  
CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
CC antibody mimics exhibit improved biophysical properties, such as  
CC stability under reducing conditions and solubility at high  
CC concentrations. In addition, these molecules are readily expressed and  
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic  
CC systems (e.g. yeast), or in vitro translation systems (e.g. rabbit  
CC reticulocyte lysate system). Furthermore, these proteins are extremely  
CC amenable to affinity maturation techniques involving multiple cycles of  
CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
CC phage display or yeast display systems. The present sequence is used in  
CC the exemplification of the present invention  
XX  
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Query Match 90.3%; Score 446; DB 5; Length 94;  
Best Local Similarity 91.5%; Pred. No. 4.2e-44;  
Matches 86; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
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DB 1 VSDVPRDLVVAAPTSLISWNRNYPARYRITYGETGNGSPVQEFVPPWASIASIS 60  
QY 61 GLKPGVDYTIITVYAVTSDTKDYKYDDPISINVRT 94  
DB 61 GLKPGADYTIITVYAVTSDTKDYKYDDPISINVRT 94

Search completed: May 18, 2005, 15:37:43  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2005, 14:57:44 ; Search time 43 Seconds  
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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pap:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	73.1	94	2	US-08-717-169-8
2	361	73.1	94	4	US-09-638-202A-110
3	361	73.1	94	4	US-09-228-901A-8
4	361	73.1	94	4	US-09-096-749A-110
5	361	73.1	94	4	US-09-637-614-110
6	361	73.1	96	4	US-09-638-202A-112
7	361	73.1	96	4	US-09-096-749A-112
8	361	73.1	96	4	US-09-637-614-112
9	361	73.1	175	1	US-08-078-683A-34
10	361	73.1	175	4	US-08-471-970A-34
11	361	73.1	175	4	US-07-723-677B-34
12	361	73.1	256	1	US-07-959-369-1
13	361	73.1	258	1	US-07-959-369-10
14	361	73.1	274	1	US-07-959-369-12
15	361	73.1	274	2	US-08-836-854-3
16	361	73.1	274	4	US-09-366-009-25
17	361	73.1	274	4	US-08-809-156B-25
18	361	73.1	277	1	US-07-959-369-3
19	361	73.1	279	1	US-07-959-369-11
20	361	73.1	279	2	US-08-836-854-8
21	361	73.1	281	1	US-07-959-369-4
22	361	73.1	283	1	US-07-959-369-13
23	361	73.1	283	2	US-08-836-854-7
24	361	73.1	302	2	US-08-836-854-5
25	361	73.1	302	4	US-09-366-009-29
26	361	73.1	302	4	US-08-809-156B-29
27	361	73.1	332	2	US-08-836-854-13

28	361	73.1	341	2	US-08-836-854-14	Sequence 14, Appl
29	361	73.1	367	2	US-08-836-854-18	Sequence 18, Appl
30	361	73.1	367	2	US-08-836-854-17	Sequence 17, Appl
31	361	73.1	383	1	US-07-959-369-5	Sequence 5, Appl
32	361	73.1	385	1	US-07-959-369-14	Sequence 14, Appl
33	361	73.1	385	2	US-08-836-854-10	Sequence 10, Appl
34	361	73.1	422	2	US-08-836-854-12	Sequence 12, Appl
35	361	73.1	432	1	US-07-959-369-8	Sequence 8, Appl
36	361	73.1	432	1	US-07-959-369-9	Sequence 9, Appl
37	361	73.1	432	2	US-08-836-854-20	Sequence 20, Appl
38	361	73.1	432	4	US-09-366-009-4	Sequence 4, Appl
39	361	73.1	432	4	US-08-809-156B-4	Sequence 4, Appl
40	361	73.1	446	2	US-08-836-854-15	Sequence 15, Appl
41	361	73.1	457	2	US-08-836-854-16	Sequence 16, Appl
42	361	73.1	457	4	US-09-366-009-5	Sequence 5, Appl
43	361	73.1	457	4	US-09-366-009-22	Sequence 22, Appl
44	361	73.1	457	4	US-08-809-156B-5	Sequence 5, Appl
45	361	73.1	457	4	US-08-809-156B-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1  
US-08-717-169-8  
; Sequence 8, Application US/08717169  
; Patent No. 5922676  
; GENERAL INFORMATION:  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Ruoslahti, Erkki  
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and  
; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronection  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/717,169  
; APPLICATION NUMBER: US/08/717,169  
; FILING DATE: 20-SEP-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2017  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-717-169-8

Query Match 73.1%; Score 361; DB 2; Length 94;  
Best Local Similarity 77.7%; Pred. No. 1.9e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

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Db 1 VSDPRDLVVAAATPSTRLLISWNSGLQSRYYRITYGTGNSPQVQETVPWASIAIIS 60

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QY 61 GLKPGVDYITTVAVTKSDTYKYDDPISINVRT 94
      |||||
Db 61 GLKPGVDYITTVAVTGRGDSPASSKPIINVRT 94

RESULT 2
US-09-638-202A-110
; Sequence 110, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-AUG-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-09-638-202A-110

Query Match 73.1%; Score 361; DB 4; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

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Db 1 VSDVPRDLVVAATPTSLRNRSGLQSYRYITYGETGNSPVQEFVPPWASITATIS 60

QY 61 GLKPGVDYITTVAVTKSDTYKYDDPISINVRT 94
      |||||
Db 61 GLKPGVDYITTVAVTGRGDSPASSKPIINVRT 94

RESULT 4
US-09-096-749A-110
; Sequence 110, Application US/09096749A
; Patent No. 6673901
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-09-096-749A-110

Query Match 73.1%; Score 361; DB 4; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLRNRSGLQSYRYITYGETGNSPVQEFVPPWASITATIS 60
      |||||
Db 1 VSDVPRDLVVAATPTSLRNRSGLQSYRYITYGETGNSPVQEFVPPWASITATIS 60

QY 61 GLKPGVDYITTVAVTKSDTYKYDDPISINVRT 94
      |||||
Db 61 GLKPGVDYITTVAVTGRGDSPASSKPIINVRT 94

RESULT 3
US-09-228-901A-8
; Sequence 8, Application US/09228901A
; Patent No. 6475488
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruoslahti, Erkki I.
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and

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; TITLE OF INVENTION: Ameliorating Cancer by Using Superfibronectin
; FILE REFERENCE: P-TX 3416
; CURRENT APPLICATION NUMBER: US/09/228,901A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 08/717,169
; PRIOR FILING DATE: 1996-09-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-228-901A-8

Query Match 73.1%; Score 361; DB 4; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLRNRSGLQSYRYITYGETGNSPVQEFVPPWASITATIS 60
      |||||
Db 1 VSDVPRDLVVAATPTSLRNRSGLQSYRYITYGETGNSPVQEFVPPWASITATIS 60

QY 61 GLKPGVDYITTVAVTKSDTYKYDDPISINVRT 94
      |||||
Db 61 GLKPGVDYITTVAVTGRGDSPASSKPIINVRT 94

RESULT 4
US-09-096-749A-110
; Sequence 110, Application US/09096749A
; Patent No. 6673901
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-09-096-749A-110

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Query Match 73.1%; Score 361; DB 4; Length 94;  
Best Local Similarity 77.7%; Pred. No. 1.9e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNSGLQSRYYRITYGETGNSPVQEFVPPWASIAIIS 60  
Db 1 VSDVPRDLEVVAAATPTSLISWNSGLQSRYYRITYGETGNSPVQEFVPPWASIAIIS 60

Qy 61 GLKEGVDYTIIVYAVTGDSPASSKPIISINRT 94  
Db 61 GLKEGVDYTIIVYAVTGDSPASSKPIISINRT 94

RESULT 5  
US-09-637-614-110  
; Sequence 110, Application US/09637614  
; Patent No. 6703199  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/637,614  
; FILING DATE: 11-Aug-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/096,749  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:

US-09-637-614-110

Query Match 73.1%; Score 361; DB 4; Length 94;  
Best Local Similarity 77.7%; Pred. No. 1.9e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNSGLQSRYYRITYGETGNSPVQEFVPPWASIAIIS 60  
Db 1 VSDVPRDLEVVAAATPTSLISWNSGLQSRYYRITYGETGNSPVQEFVPPWASIAIIS 60

Qy 61 GLKEGVDYTIIVYAVTGDSPASSKPIISINRT 94  
Db 61 GLKEGVDYTIIVYAVTGDSPASSKPIISINRT 94

RESULT 6  
US-09-638-202A-112  
; Sequence 112, Application US/09638202A  
; Patent No. 6462189  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/638,202A  
; FILING DATE: 11-Aug-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/096,749  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 112:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 96 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:

US-09-638-202A-112

Query Match 73.1%; Score 361; DB 4; Length 96;  
Best Local Similarity 77.7%; Pred. No. 2e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNSGLQSRYYRITYGETGNSPVQEFVPPWASIAIIS 60  
Db 3 VSDVPRDLEVVAAATPTSLISWNSGLQSRYYRITYGETGNSPVQEFVPPWASIAIIS 62

Qy 61 GLKEGVDYTIIVYAVTGDSPASSKPIISINRT 94  
Db 63 GLKEGVDYTIIVYAVTGDSPASSKPIISINRT 96

RESULT 7  
US-09-096-749A-112  
; Sequence 112, Application US/09096749A  
; Patent No. 6673901  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN



FRAGMENT TYPE: internal  
US-08-078-683A-34

Query Match 73.1%; Score 361; DB 1; Length 175;  
Best Local Similarity 77.7%; Pred. No. 4.4e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGTGNSPVQVETVPWASIIATIS 60  
Db 82 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGTGNSPVQVETVPWASIIATIS 141  
Qy 61 GLKPGVDYITVYAVTKSDTYKYDDPISINVRT 94  
Db 142 GLKPGVDYITVYAVTGRGDSPASSKPIISINVRT 175

## RESULT 10

US-08-471-970A-34

; Sequence 34, Application US/08471970A

; Patent No. 6531295

; GENERAL INFORMATION:

; APPLICANT: Saunders, Scott

; APPLICANT: Bernfield, Merton

; APPLICANT: Kato, Masato

; TITLE OF INVENTION: Construction and Use of Synthetic

; TITLE OF INVENTION: Constructs Encoding Syndecan

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII (text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,970A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/078,683

; FILING DATE: 17-JUN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Kara, Catherine J.

; REGISTRATION NUMBER: P-41,106

; REFERENCE/DOCKET NUMBER: CME-062DV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 175 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-471-970A-34

Query Match 73.1%; Score 361; DB 4; Length 175;  
Best Local Similarity 77.7%; Pred. No. 4.4e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGTGNSPVQVETVPWASIIATIS 60  
Db 82 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGTGNSPVQVETVPWASIIATIS 141

Qy 61 GLKPGVDYITVYAVTKSDTYKYDDPISINVRT 94

Db 142 GLKPGVDYITVYAVTGRGDSPASSKPIISINVRT 175

## RESULT 11

US-09-723-677B-34

; Sequence 34, Application US/09723677B

; Patent No. 6699568

; GENERAL INFORMATION:

; APPLICANT: SAUNDERS, SCOTT

; APPLICANT: BERNFIELD, MERTON

; APPLICANT: KATO, MASATO

; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN

; FILE REFERENCE: 101353-151

; CURRENT APPLICATION NUMBER: US/09/723,677B

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 08/471,970

; PRIOR FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: 08/078,683

; PRIOR FILING DATE: 1993-06-17

; PRIOR APPLICATION NUMBER: 07/856,869

; PRIOR FILING DATE: 1992-03-24

; PRIOR APPLICATION NUMBER: 07/757,654

; PRIOR FILING DATE: 1991-09-06

; PRIOR APPLICATION NUMBER: 07/746,797

; PRIOR FILING DATE: 1991-08-12

; PRIOR APPLICATION NUMBER: 07/331,585

; PRIOR FILING DATE: 1989-03-29

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 34

; LENGTH: 175

; TYPE: PRT

; ORGANISM: MUS SP;HOMO SAPIEN

US-09-723-677B-34

Query Match 73.1%; Score 361; DB 4; Length 175;

Best Local Similarity 77.7%; Pred. No. 4.4e-35;

Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGTGNSPVQVETVPWASIIATIS 60  
Db 82 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGTGNSPVQVETVPWASIIATIS 141

Qy 61 GLKPGVDYITVYAVTKSDTYKYDDPISINVRT 94

Db 142 GLKPGVDYITVYAVTGRGDSPASSKPIISINVRT 175

## RESULT 12

US-07-959-369-1

; Sequence 1, Application US/07959369

; Patent No. 5302701

; GENERAL INFORMATION:

; APPLICANT: Hidetaka HASHI et al.

; TITLE OF INVENTION: No. 5302701e1 Functional Polypeptide

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/959,369

; FILING DATE: 19921013

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:



;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek, Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX:  
;; TELEX:

;; INFORMATION FOR SEQ ID NO: 1:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 256 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: polypeptide  
;; HYPOTHETICAL:  
;; ANTI-SENSE:  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; ORGANISM:

;; STRAIN:  
;; INDIVIDUAL ISOLATE:  
;; DEVELOPMENTAL STAGE:  
;; HAPLOTYPE:  
;; TISSUE TYPE:  
;; CELL TYPE:  
;; CELL LINE:  
;; ORGANELLE:  
;; IMMEDIATE SOURCE:  
;; LIBRARY:

;; CLONE:  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT:  
;; MAP POSITION:  
;; UNITS:  
;; FEATURE:

;; NAME/KEY:  
;; LOCATION:  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION:  
;; PUBLICATION INFORMATION:  
;; AUTHORS:  
;; TITLE:  
;; JOURNAL:  
;; VOLUME:  
;; ISSUE:  
;; PAGES:  
;; DATE:

;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:  
;; RELEVANT RESIDUES IN SEQ ID NO:  
US-07-959-369-1

Query Match 73.1%; Score 361; DB 1; Length 256;  
Best Local Similarity 77.7%; Pred. No. 7.2e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISMNRSGLQSKRYRITYGETGNSPVQSEFTVPPWASIAIIS 60  
Db 157 VSDVPRDLEVAATPTSLISWDAPAVTVYRITYGETGNSPVQSEFTVPGSKSTATIS 216  
QY 61 GLKPGVDYITTVYAVTKSDTYKYDDPISINVRT 94  
Db 217 GLKPGVDYITTVYAVTGRGDSPASSKPIINVRT 250

RESULT 13  
US-07-959-369-10  
; Sequence 10, Application US/07959369  
; Patent No. 5302701  
; GENERAL INFORMATION:

;; APPLICANT: Hidetaka HASHI et al.  
;; TITLE OF INVENTION: No. 5302701el Functional Polypeptide  
;; NUMBER OF SEQUENCES: 23  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wenderoth, Lind & Ponack  
;; STREET: 805 Fifteenth Street, N.W., #700  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/959,369  
;; FILING DATE: 19921013  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warren M. Cheek, Jr.  
;; REGISTRATION NUMBER: 33,367  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-8850  
;; TELEFAX:  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 258 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: polypeptide  
;; HYPOTHETICAL:  
;; ANTI-SENSE:  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; ORGANISM:  
;; STRAIN:  
;; INDIVIDUAL ISOLATE:  
;; DEVELOPMENTAL STAGE:  
;; HAPLOTYPE:  
;; TISSUE TYPE:  
;; CELL TYPE:  
;; CELL LINE:  
;; ORGANELLE:  
;; IMMEDIATE SOURCE:  
;; LIBRARY:  
;; CLONE:  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT:  
;; MAP POSITION:  
;; UNITS:  
;; FEATURE:  
;; NAME/KEY:  
;; LOCATION:  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION:  
;; PUBLICATION INFORMATION:  
;; AUTHORS:  
;; TITLE:  
;; JOURNAL:  
;; VOLUME:  
;; ISSUE:  
;; PAGES:  
;; DATE:  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:

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; RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-10
Query Match 73.1%; Score 361; DB 1; Length 258;
Best Local Similarity 77.7%; Pred. No. 7.3e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLQSRVYRITYGETGNSPVQEFVPPWASIATIS 60
Db 157 VSDVPRDLEVVAAATPTSLISWDAPAVTVYRITYGETGNSPVQEFVPGSKSTATIS 216
Qy 61 GLKPGVDYTTIVYAVTDKSDTKYDDPISINVRT 94
Db 217 GLKPGVDYTTIVYAVTGRGDSPASSKPI SINVRT 250

RESULT 14
US-07-959-369-12
; Sequence 12, Application US/07959369
; Patent No. 5302701
; GENERAL INFORMATION:
; APPLICANT: Hidetaka HASHI et al.
; TITLE OF INVENTION: No. 5302701el Functional Polypeptide
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,369
; FILING DATE: 19921013
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:

; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-12
Query Match 73.1%; Score 361; DB 1; Length 274;
Best Local Similarity 77.7%; Pred. No. 7.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLQSRVYRITYGETGNSPVQEFVPPWASIATIS 60
Db 178 VSDVPRDLEVVAAATPTSLISWDAPAVTVYRITYGETGNSPVQEFVPGSKSTATIS 237
Qy 61 GLKPGVDYTTIVYAVTDKSDTKYDDPISINVRT 94
Db 238 GLKPGVDYTTIVYAVTGRGDSPASSKPI SINVRT 271

RESULT 15
US-08-836-854-3
; Sequence 3, Application US/08836854
; Patent No. 5824547
; GENERAL INFORMATION:
; APPLICANT: HASHINO, Kimikazu
; APPLICANT: MATSUSHITA, Hideyuki
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/02425
; FILING DATE: 29-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 317721/1994
; FILING DATE: 29-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: HASHINO=1
```

;  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 274 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-836-854-3

Query Match 73.1%; Score 361; DB 2; Length 274;  
Best Local Similarity 77.7%; Pred. No. 7.9e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 VSDVPRDLEVAATPTSLRLISWNRGLQSRYYRITYGETGNSPVQEFVPPWASIATIS 60  
Db 178 VSDVPRDLEVAATPTSLRLISWNRGLQSRYYRITYGETGNSPVQEFVPPWASIATIS 237  
  
QY 61 GLKPGVDYITIVYAVTGRGDSPPASSXPISINVRT 94  
Db 238 GLKPGVDYITIVYAVTGRGDSPPASSXPISINVRT 271

Search completed: May 18, 2005, 15:31:48  
Job time : 44 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2005, 15:35:03 ; Search time 134 Seconds  
(without alignments)  
234.655 Million cell updates/sec

Title: US-09-688-566-81  
Perfect score: 494  
Sequence: 1 VSDVPRDLEVVAAVPTSLRI.....VTDKSDTYKYDDPISINRYT 94

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	367.5	74.4	96	14	US-10-302-456-1
2	361	73.1	94	9	US-09-096-749A-110
3	361	73.1	94	14	US-10-174-717A-110
4	361	73.1	94	14	US-10-165-155-110
5	361	73.1	94	14	US-10-190-162-110
6	361	73.1	96	9	US-09-096-749A-112
7	361	73.1	96	10	US-09-903-412-110
8	361	73.1	96	10	US-09-903-412-112
9	361	73.1	96	10	US-09-903-412-121
10	361	73.1	96	14	US-10-174-717A-112
11	361	73.1	96	14	US-10-165-155-112
12	361	73.1	96	14	US-10-190-162-112
13	361	73.1	96	14	US-10-006-760-2

14	361	73.1	175	17	US-10-776-989-34	Sequence 34, Appl
15	361	73.1	274	10	US-09-775-964-25	Sequence 25, Appl
16	361	73.1	274	17	US-10-486-512-1	Sequence 1, Appl
17	361	73.1	302	17	US-09-775-964-29	Sequence 29, Appl
18	361	73.1	302	17	US-10-486-512-7	Sequence 7, Appl
19	361	73.1	330	14	US-10-279-733-10	Sequence 10, Appl
20	361	73.1	367	17	US-10-486-512-8	Sequence 8, Appl
21	361	73.1	368	17	US-10-486-512-9	Sequence 9, Appl
22	361	73.1	370	17	US-10-486-512-10	Sequence 10, Appl
23	361	73.1	432	10	US-09-775-964-4	Sequence 4, Appl
24	361	73.1	457	10	US-09-775-964-5	Sequence 5, Appl
25	361	73.1	457	10	US-09-775-964-22	Sequence 22, Appl
26	361	73.1	457	17	US-10-486-512-11	Sequence 11, Appl
27	361	73.1	464	10	US-09-775-964-7	Sequence 7, Appl
28	361	73.1	472	10	US-09-775-964-21	Sequence 21, Appl
29	361	73.1	472	17	US-10-486-512-12	Sequence 12, Appl
30	361	73.1	489	10	US-09-775-964-8	Sequence 8, Appl
31	361	73.1	549	10	US-09-775-964-23	Sequence 23, Appl
32	361	73.1	549	17	US-10-486-512-5	Sequence 5, Appl
33	361	73.1	574	10	US-09-775-964-24	Sequence 24, Appl
34	361	73.1	574	17	US-10-486-512-6	Sequence 6, Appl
35	361	73.1	599	14	US-10-279-733-9	Sequence 9, Appl
36	361	73.1	826	10	US-09-775-964-14	Sequence 14, Appl
37	361	73.1	847	16	US-10-741-601-361	Sequence 361, App
38	361	73.1	847	17	US-10-741-600-1073	Sequence 1073, Ap
39	361	73.1	1259	16	US-10-741-601-365	Sequence 365, App
40	361	73.1	1259	17	US-10-741-600-1077	Sequence 1077, Ap
41	361	73.1	1286	16	US-10-741-601-362	Sequence 362, App
42	361	73.1	1286	17	US-10-741-600-1074	Sequence 1074, Ap
43	361	73.1	1315	16	US-10-741-601-358	Sequence 358, App
44	361	73.1	1315	17	US-10-741-600-1068	Sequence 1068, Ap
45	361	73.1	1341	16	US-10-741-601-355	Sequence 355, App

ALIGNMENTS

RESULT 1  
US-10-302-456-1  
; Sequence 1, Application US/10302456  
; Publication No. US20030100004A1  
; GENERAL INFORMATION:  
; APPLICANT: Kurz, Markus  
; TITLE OF INVENTION: Solid Phase Immobilization of Proteins  
; TITLE OF INVENTION: and Peptides  
; FILE REFERENCE: 50036/051002  
; CURRENT APPLICATION NUMBER: US/10302,456  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 60/333,470  
; PRIOR FILING DATE: 2001-11-27  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-302-456-1

Query Match 74.4%; Score 367.5; DB 14; Length 96;  
Best Local Similarity 80.0%; Pred. No. 4.5e-34;  
Matches 76; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

Qy	1	VSDVPRDLEVVAAVPTSLRI...VTDKSDTYKYDDPISINRYT 94
Db	2	VSDVPRDLEVVAAVPTSLRI...VTDKSDTYKYDDPISINRYT 96
Qy	61	GLKPGVDYTTIVYAVTDKSDT-YKYDDPISINRYT 94
Db	62	GLKPGVDYTTIVYAVTDKSDT-YKYDDPISINRYT 96

RESULT 2  
US-09-096-749A-110  
; Sequence 110, Application US/09096749A  
; Patent No. US20020019517A1  
; GENERAL INFORMATION:  
; APPLICANT: Koleda, Shohel  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749A  
; FILING DATE: June 12, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; FILING DATE:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-09-096-749A-110

Query Match 73.1%; Score 361; DB 9; Length 94;  
Best Local Similarity 77.7%; Pred. No. 2.4e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYTGETGNSPVQSEFTVPPWASTATIS 60  
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYTGETGNSPVQSEFTVPPWASTATIS 60  
QY 61 GLKPGVDYITVYAVTKSDTKYDDPISINVRT 94  
Db 61 GLKPGVDYITVYAVTGRGDSPASSKPIINVRT 94

US-09-096-749A-110

Query Match 73.1%; Score 361; DB 9; Length 94;  
Best Local Similarity 77.7%; Pred. No. 2.4e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYTGETGNSPVQSEFTVPPWASTATIS 60  
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYTGETGNSPVQSEFTVPPWASTATIS 60  
QY 61 GLKPGVDYITVYAVTKSDTKYDDPISINVRT 94  
Db 61 GLKPGVDYITVYAVTGRGDSPASSKPIINVRT 94

RESULT 3  
US-10-174-717A-110  
; Sequence 110, Application US/1017417A  
; Publication No. US20030108948A1  
; APPLICANT: Koleda, Shohel  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, St. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: FastSEQ Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/174,717A  
FILING DATE: 18-Jun-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/096,749  
FILING DATE: June 12, 1998  
APPLICATION NUMBER: 60/049,410  
FILING DATE: June 12, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ann S. Viksnins  
REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 109.034US4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 373-6900  
TELEFAX: (612) 339-3061  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 94 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 110:  
US-10-174-717A-110

Query Match 73.1%; Score 361; DB 14; Length 94;  
Best Local Similarity 77.7%; Pred. No. 2.4e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYTGETGNSPVQSEFTVPPWASTATIS 60  
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYTGETGNSPVQSEFTVPPWASTATIS 60  
QY 61 GLKPGVDYITVYAVTKSDTKYDDPISINVRT 94  
Db 61 GLKPGVDYITVYAVTGRGDSPASSKPIINVRT 94

RESULT 4  
US-10-165-155-110  
; Sequence 110, Application US/10165155  
; Publication No. US20030134386A1  
; GENERAL INFORMATION:  
; APPLICANT: Koleda, Shohel  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/165,155  
; FILING DATE: 06-Jun-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749  
; FILING DATE: June 12, 1998

Qy 1 VSDVPRDLVWAATPTSLRISWNRSGLQSRYYRITYGETGCNSPVQEFYPPWASIAIS 60

Db 3 VSDVPRDLEVAATPTSLLSWDAPAVTVRYRYITYGETGNSPVQEFVTPGSKSTATIS 62

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94  
||||| : | : |||||

Db 63 GLKPGVDYITTVYAVTGRGDSPASSKPISINVRT 96  
||||| : | : |||||

RESULT 7

US-09-903-412-110

; Sequence 110, Application US/09903412

; Publication No. US20030027319A1

; GENERAL INFORMATION:

; APPLICANT: Koide, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; FILE REFERENCE: 109.050US1

; CURRENT APPLICATION NUMBER: US/09/903,412

; CURRENT FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: US 60/217,474

; PRIOR FILING DATE: 2000-07-11

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 110

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The synthetic Fn3 gene.

US-09-903-412-110

Query Match 73.1%; Score 361; DB 10; Length 96;

Best Local Similarity 77.7%; Pred. No. 2.5e-33;

Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLLSWDAPAVTVRYRYITYGETGNSPVQEFVTPGSKSTATIS 60  
||||| : | : |||||

Db 3 VSDVPRDLEVAATPTSLLSWDAPAVTVRYRYITYGETGNSPVQEFVTPGSKSTATIS 62  
||||| : | : |||||

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94  
||||| : | : |||||

Db 63 GLKPGVDYITTVYAVTGRGDSPASSKPISINVRT 96  
||||| : | : |||||

RESULT 8

US-09-903-412-112

; Sequence 112, Application US/09903412

; Publication No. US20030027319A1

; GENERAL INFORMATION:

; APPLICANT: Koide, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; FILE REFERENCE: 109.050US1

; CURRENT APPLICATION NUMBER: US/09/903,412

; CURRENT FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: US 60/217,474

; PRIOR FILING DATE: 2000-07-11

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 112

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The designed Fn3 gene.

US-09-903-412-112

Query Match 73.1%; Score 361; DB 10; Length 96;

Best Local Similarity 77.7%; Pred. No. 2.5e-33;

Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLLSWDAPAVTVRYRYITYGETGNSPVQEFVTPGSKSTATIS 60  
||||| : | : |||||

Db 3 VSDVPRDLEVAATPTSLLSWDAPAVTVRYRYITYGETGNSPVQEFVTPGSKSTATIS 62  
||||| : | : |||||

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94  
||||| : | : |||||

Db 63 GLKPGVDYITTVYAVTGRGDSPASSKPISINVRT 96  
||||| : | : |||||

Db 63 GLKPGVDYITTVYAVTGRGDSPASSKPISINVRT 96  
||||| : | : |||||

RESULT 9

US-09-903-412-121

; Sequence 121, Application US/09903412

; Publication No. US20030027319A1

; GENERAL INFORMATION:

; APPLICANT: Koide, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; FILE REFERENCE: 109.050US1

; CURRENT APPLICATION NUMBER: US/09/903,412

; CURRENT FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: US 60/217,474

; PRIOR FILING DATE: 2000-07-11

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 121

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-903-412-121

Query Match 73.1%; Score 361; DB 10; Length 96;

Best Local Similarity 77.7%; Pred. No. 2.5e-33;

Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLLSWDAPAVTVRYRYITYGETGNSPVQEFVTPGSKSTATIS 60  
||||| : | : |||||

Db 3 VSDVPRDLEVAATPTSLLSWDAPAVTVRYRYITYGETGNSPVQEFVTPGSKSTATIS 62  
||||| : | : |||||

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94  
||||| : | : |||||

Db 63 GLKPGVDYITTVYAVTGRGDSPASSKPISINVRT 96  
||||| : | : |||||

RESULT 10

US-10-174-717A-112

; Sequence 112, Application US/10174717A

; Publication No. US20030108948A1

; APPLICANT: Koide, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; NUMBER OF SEQUENCES: 118

; CORRESPONDENCE ADDRESS:

; ADDRESS: Schwegman, Lundberg, Woessner & Kluth P.A.

; STREET: 121 South Eighth Street, St. 1600

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: WINDOWS

SOFTWARE: FastSeq Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/174,717A

FILING DATE: 18-Jun-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/096,749

FILING DATE: June 12, 1998

APPLICATION NUMBER: 60/049,410

FILING DATE: June 12, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ann S. Viksnins

REGISTRATION NUMBER: 37,748

REFERENCE/DOCKET NUMBER: 109.034US4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 373-6900

TELEFAX: (612) 339-3061

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:



LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-10-174-717A-112

Query Match 73.1%; Score 361; DB 14; Length 96;  
Best Local Similarity 77.7%; Pred. No. 2.5e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
Qy 1 VSDVPRDLEVAATPTSLRISWNSRGLQSRYYRITYGETGNSPVQVETVPWASIATIS 60  
Db 3 VSDVPRDLEVAATPTSLRISWNSRGLQSRYYRITYGETGNSPVQVETVPWASIATIS 62  
Qy 61 GLKPGVDYTIIVAVTGDSPASSKPISINVRT 94  
Db 63 GLKPGVDYTIIVAVTGDSPASSKPISINVRT 96

RESULT 11  
US-10-165-155-112  
; Sequence 112, Application US/10165155  
; Publication No. US20030134386A1  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/165,155  
; FILING DATE: 06-Jun-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749  
; FILING DATE: June 12, 1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Vikens  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 112:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 96 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-10-165-155-112

Query Match 73.1%; Score 361; DB 14; Length 96;

Best Local Similarity 77.7%; Pred. No. 2.5e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
Qy 1 VSDVPRDLEVAATPTSLRISWNSRGLQSRYYRITYGETGNSPVQVETVPWASIATIS 60  
Db 3 VSDVPRDLEVAATPTSLRISWNSRGLQSRYYRITYGETGNSPVQVETVPWASIATIS 62  
Qy 61 GLKPGVDYTIIVAVTGDSPASSKPISINVRT 94  
Db 63 GLKPGVDYTIIVAVTGDSPASSKPISINVRT 96

RESULT 12  
US-10-190-162-112  
; Sequence 112, Application US/10190162  
; Publication No. US20030170753A1  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/190,162  
; FILING DATE: 03-Jul-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749  
; FILING DATE: June 12, 1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Vikens  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 112:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 96 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-10-190-162-112

Query Match 73.1%; Score 361; DB 14; Length 96;  
Best Local Similarity 77.7%; Pred. No. 2.5e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
Qy 1 VSDVPRDLEVAATPTSLRISWNSRGLQSRYYRITYGETGNSPVQVETVPWASIATIS 60  
Db 3 VSDVPRDLEVAATPTSLRISWNSRGLQSRYYRITYGETGNSPVQVETVPWASIATIS 62  
Qy 61 GLKPGVDYTIIVAVTGDSPASSKPISINVRT 94  
Db 63 GLKPGVDYTIIVAVTGDSPASSKPISINVRT 96

RESULT 13

US-10-006-760-2  
; Sequence 2, Application US/10006760  
; Publication No. US20030186385A1  
; GENERAL INFORMATION:  
; APPLICANT: Koide, Shohel  
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND  
; TO TARGET PROTEINS AND USE THEREOF  
; FILE REFERENCE: 176/60901  
; CURRENT APPLICATION NUMBER: US/10/006,760  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/249,756  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-006-760-2

Query Match 73.1%; Score 361; DB 14; Length 96;  
Best Local Similarity 77.7%; Pred. No. 2.5e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
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DB 3 VSDVPRDLEVVAATPTSLISWDAAPVTVRYRITYGETGNSPVQEFVPPWASITATIS 62  
QY 61 GLKPGVDYITVYAVTCKSDTYKYDDPISINVRT 94  
DB 63 GLKPGVDYITVYAVTGRGDSPPASSKPISINVRT 96

RESULT 14  
US-10-776-989-34  
; Sequence 34, Application US/10776989  
; Publication No. US20050075484A1  
; GENERAL INFORMATION:  
; APPLICANT: SAUNDERS, SCOTT  
; APPLICANT: BERNFIELD, MERTON  
; APPLICANT: KATO, MASATO  
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN  
; FILE REFERENCE: 101353-232  
; CURRENT APPLICATION NUMBER: US/10/776,989  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 09/723,677  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 08/471,970  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 08/078,683  
; PRIOR FILING DATE: 1993-06-17  
; PRIOR APPLICATION NUMBER: 07/856,869  
; PRIOR FILING DATE: 1992-03-24  
; PRIOR APPLICATION NUMBER: 07/757,654  
; PRIOR FILING DATE: 1991-09-06  
; PRIOR APPLICATION NUMBER: 07/746,797  
; PRIOR FILING DATE: 1991-08-12  
; PRIOR APPLICATION NUMBER: 07/331,585  
; PRIOR FILING DATE: 1989-03-29  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: MUS SP;HOMO SAPIEN  
US-10-776-989-34

Query Match 73.1%; Score 361; DB 17; Length 175;  
Best Local Similarity 77.7%; Pred. No. 5.1e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
QY 1 VSDVPRDLEVVAATPTSLISWDAAPVTVRYRITYGETGNSPVQEFVPPWASITATIS 60

DB 82 VSDVPRDLEVVAATPTSLISWDAAPVTVRYRITYGETGNSPVQEFVPPWASITATIS 141  
QY 61 GLKPGVDYITVYAVTCKSDTYKYDDPISINVRT 94  
DB 142 GLKPGVDYITVYAVTGRGDSPPASSKPISINVRT 175  
RESULT 15  
US-09-775-964-25  
; Sequence 25, Application US/09775964  
; Publication No. US20030087437A1  
; GENERAL INFORMATION:  
; APPLICANT: Asada, Kiyozo  
; Uemori, Takashi  
; Koyama, No. US20030087437A1  
; Hashino, Kimikazu  
; Kato, Ikunoshin  
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET  
; CELLS WITH RETROVIRUS  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WEISER & ASSOCIATES  
; STREET: 230 South Fifteenth Street, Suite 500  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/775,964  
FILING DATE: 20-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/366,009  
FILING DATE: 02-Aug-1999  
APPLICATION NUMBER: 08/809,156  
FILING DATE: <Unknown>  
APPLICATION NUMBER: JP 294382/1995  
FILING DATE: 13-NOV-1995  
APPLICATION NUMBER: JP 051847/1996  
FILING DATE: 08-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 977.6507P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 274 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-775-964-25

Query Match 73.1%; Score 361; DB 10; Length 274;  
Best Local Similarity 77.7%; Pred. No. 8.9e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
QY 1 VSDVPRDLEVVAATPTSLISWDAAPVTVRYRITYGETGNSPVQEFVPPWASITATIS 60  
DB 178 VSDVPRDLEVVAATPTSLISWDAAPVTVRYRITYGETGNSPVQEFVPPWASITATIS 237  
QY 61 GLKPGVDYITVYAVTCKSDTYKYDDPISINVRT 94

Db 238 GLKPGVDYTIIVYAVTGRGDSPASSKPISINVRT 271

Search completed: May 18, 2005, 15:50:05  
Job time : 135 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2005, 15:31:59 ; Search time 40 Seconds  
(without alignments)  
226,109 Million cell updates/sec

Title: US-09-688-566-81  
Perfect score: 494  
Sequence: 1 VSDVPRDLVVAAPTSLI.....VTDKSDTYKYDDPISINVRT 94

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: Piri: \*  
2: Piri2: \*  
3: Piri3: \*  
4: Piri4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	73.1	2386	1 FNHU	fibronectin precu
2	354	71.7	2265	1 FNBO	fibronectin - bovi
3	333	67.4	2477	2 S14428	fibronectin precu
4	311	63.0	273	2 A28512	fibronectin - chic
5	311	63.0	1020	2 A29355	fibronectin - chic
6	262	53.0	2481	2 A43908	fibronectin - Afri
7	125	25.3	4006	2 T09070	probable tenascin
8	124	25.1	4135	2 T42629	tenascin-X - bovin
9	121	24.5	1353	1 JH0675	restricrin precurs
10	121	24.5	1746	1 S19694	tenascin precursor
11	116	23.5	1356	2 A45445	janusin precursor,
12	111	22.5	3566	1 A40701	tenascin-X precurs
13	110.5	22.4	1898	2 S46216	leukocyte antigen-
14	110	22.3	2019	1 J01322	tenascin precursor
15	108	21.9	933	2 A1930	cytotactin - chick
16	108	21.9	1810	1 A32230	tenascin precursor
17	106.5	21.6	2944	2 A54849	collagen alpha 1(V
18	105	21.3	2201	2 A32160	tenascin-C - pig
19	102	20.6	417	2 S65944	tenascin-X - huan
20	100	20.2	1912	2 A56178	protein-tyrosine-p
21	98.5	19.9	647	2 A43902	tenascin - eastern
22	96	19.4	1290	2 A56493	leucocyte common a
23	96	19.4	3124	2 A40020	collagen alpha 1(X
24	94	19.0	843	2 A40970	undulin 1 - human
25	92	18.6	1691	1 D54689	protein-tyrosine-p
26	92	18.6	1894	2 C54689	protein-tyrosine-p
27	91.5	18.5	147	2 S00848	fibronectin, trans
28	90.5	18.3	440	2 I50213	protein-tyrosine-p
29	88.5	17.9	189	2 S71465	fibronectin - chic

30	88.5	17.9	575	2 A54861	tenascin - rat (fr
31	87.5	17.7	90	2 I46162	fibronectin ED-B -
32	87	17.6	1897	1 TDHULK	leukocyte antigen-
33	86	17.4	1711	1 A55148	protein-tyrosine-p
34	83	16.8	860	2 I48839	tenascin-X - mouse
35	82	16.6	89	2 I46161	fibronectin ED-A -
36	82	16.6	1241	2 T37190	nephrit - human
37	81.5	16.5	929	2 I51027	type XII collagen
38	81.5	16.5	1747	2 A45974	collagen alpha 1(X
39	81.5	16.5	1857	2 S31212	collagen alpha 1(X
40	81.5	16.5	1888	2 S78476	collagen alpha 1(X
41	80	16.2	1914	2 T42635	tenascin Y precurs
42	79	16.0	2029	1 TDFELK	protein-tyrosine-p
43	78	15.8	1337	1 I38670	protein-tyrosine-p
44	77.5	15.7	445	2 B40970	undulin 2 - human
45	77	15.6	725	2 A90255	hypothetical prote

ALIGNMENTS

RESULT 1

FNHU  
N:Alternate names: fibronectin splice form ED-A  
C:Species: Homo sapiens (man)  
C:Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 09-Jul-2004  
C:Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22  
R:Dean, D.C.; Bowlin, C.L.; Bourgeois, S.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987  
A:Title: Cloning and analysis of the promoter region of the human fibronectin gene.  
A:Reference number: A26460; MUID:87175578; PMID:3031656  
A:Accession: A26460  
A:Molecule type: DNA  
A:Residues: 1-49 <DEA>  
A:Cross-references: UNIPROT:P02751; UNIPROT:Q14327; GB:M15801; NID:G182686; PIDN:AAAS337  
R:Oldberg, A.; Ruoslahti, E.  
J. Biol. Chem. 261, 2113-2116, 1986  
A:Title: Evolution of the fibronectin gene.  
A:Reference number: A26284; MUID:86111901; PMID:3003095  
A:Accession: A26284  
A:Molecule type: DNA  
A:Residues: 1447-1540 <OLD>  
A:Cross-references: GB:M12549; NID:G182688  
R:Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.  
Nucleic Acids Res. 16, 3545-3557, 1988  
A:Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B  
A:Reference number: S00848; MUID:88233940; PMID:3375063  
A:Accession: S03917  
A:Molecule type: DNA  
A:Residues: 1594-1767, 'V', 1769-1783 <PAO>  
A:Cross-references: EMBL:X07718; NID:G31402  
A:Note: the authors translated the codon AAC for residue 1631 as Asp  
R:Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.  
FEBS Lett. 207, 287-291, 1986  
A:Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:  
A:Reference number: A24854; MUID:87030929; PMID:3770201  
A:Accession: A24854  
A:Molecule type: DNA  
A:Residues: 1992-2147 <VIB>  
A:Cross-references: GB:X04530; NID:G31436  
R:Gutman, A.; Yamada, K.M.; Kornblihtt, A.  
FEBS Lett. 207, 145-148, 1986  
A:Title: Human fibronectin is synthesized as a pre-propolypeptide.  
A:Reference number: A24476; MUID:87030890; PMID:3770189  
A:Accession: A24476  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-14, 'Q', 16-38 <GUT>  
R:Kornblihtt, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.  
EMBO J. 4, 1755-1759, 1985  
A:Title: Primary structure of human fibronectin: differential splicing may generate at l

A;Reference number: A91008; MUID:85284965; PMID:2992939  
 A;Accession: A91008  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 32-1344;1346-2080;2112-2386 <KOR>  
 A;Cross-references: GB:X02761  
 R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.  
 Nucleic Acids Res. 12, 5853-5868, 1984  
 A;Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptide  
 A;Reference number: A93529; MUID:84272258; PMID:6462919  
 A;Accession: A93529  
 A;Molecule type: mRNA  
 A;Residues: 973-2080;2112-2386 <K02>  
 A;Cross-references: GB:X00739  
 R;Oldberg, A.; Linney, E.; Ruoslahti, E.  
 J. Biol. Chem. 258, 10193-10196, 1983  
 A;Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a  
 A;Reference number: A21011; MUID:83290929; PMID:6668418  
 A;Accession: A21011  
 A;Molecule type: mRNA  
 A;Residues: 1434-1537 <OL2>  
 A;Cross-references: GB:X00055; NID:gl82680; PIDN:AAA52459.1; PID:gl82683  
 R;Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.  
 Biochemistry 24, 2698-2704, 1985  
 A;Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra  
 A;Reference number: A90495; MUID:85280409; PMID:2592573  
 A;Accession: A90495  
 A;Molecule type: mRNA  
 A;Residues: 1594-2386 <BER>  
 A;Cross-references: GB:M10905; NID:gl82696; PIDN:AAA52462.1; PID:gl82697  
 R;Umezawa, K.; Kornblitt, A.R.; Baralle, F.E.  
 FEBS Lett. 196, 31-34, 1985  
 A;Title: Isolation and characterization of cDNA clones for human liver fibronectin.  
 A;Reference number: A22245; MUID:85231203; PMID:2989004  
 A;Accession: A22245  
 A;Molecule type: mRNA  
 A;Residues: 1948-2067 <UME>  
 A;Cross-references: GB:M27589; NID:gl82705; PIDN:AAA52465.1; PID:gl82706  
 A;Accession: B22245  
 A;Molecule type: mRNA  
 A;Residues: 1975-1991;2017-2039 <UM2>  
 A;Cross-references: GB:M27590  
 R;Sekiguchi, K.; Klob, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.  
 Biochemistry 25, 4936-4941, 1986  
 A;Title: Human liver fibronectin complementary DNAs: identification of two different mes  
 A;Reference number: I52394; MUID:87026578; PMID:3021206  
 A;Accession: I65273  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 <SEK>  
 A;Cross-references: GB:M14060; NID:gl82701; PIDN:AAA52464.1; PID:gl82704  
 R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983  
 A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectin  
 A;Reference number: A21165; MUID:83221567; PMID:6304699  
 A;Accession: A21165  
 A;Molecule type: mRNA  
 A;Residues: 2291-2386 <K03>  
 A;Cross-references: GB:K00799; NID:gl82681; PIDN:AAA52460.1; PID:gl82684  
 R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.  
 J. Biol. Chem. 258, 12670-12674, 1983  
 A;Title: Primary structure of human plasma fibronectin.  
 A;Reference number: A92398; MUID:84032463; PMID:6630202  
 A;Accession: A92398  
 A;Molecule type: protein  
 A;Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>  
 R;Garcia-Pardo, A.; Gold, L.I.  
 Arch. Biochem. Biophys. 304, 181-188, 1993  
 A;Title: Further characterization of the binding of fibronectin to gelatin reveals the fi  
 A;Reference number: S34791; MUID:93312001; PMID:8323285  
 A;Accession: S34791  
 A;Molecule type: protein  
 A;Residues: 291-300;551-560 <GAR2>

R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.  
 Thromb. Res. 43, 469-477, 1986  
 A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.  
 A;Reference number: A60904; MUID:87019725; PMID:3532418  
 A;Accession: A60904  
 A;Molecule type: protein  
 A;Residues: 293-301 <GRI>  
 R;Calaycay, J.; Pande, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.  
 J. Biol. Chem. 260, 12136-12141, 1985  
 A;Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pl  
 A;Reference number: A23901; MUID:86008277; PMID:3900070  
 A;Accession: A23901  
 A;Molecule type: protein  
 A;Residues: 616-677, 'O', 679-703, 'PT' <CAL>  
 R;Pierschbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.  
 J. Biol. Chem. 257, 9593-9597, 1982  
 A;Title: The cell attachment domain of fibronectin. Determination of the primary struct  
 A;Reference number: A92386; MUID:82265604; PMID:7050098  
 A;Accession: A92386  
 A;Molecule type: protein  
 A;Residues: 1441-1548 <PIB>  
 A;Note: residues 1524-1527 are responsible for the cell-binding activity  
 R;Garcia-Pardo, A.; Rostagno, A.; Frangione, B.  
 Biochem. J. 241, 923-928, 1987  
 A;Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dom  
 A;Reference number: A32517; MUID:87241275; PMID:3593230  
 A;Accession: A32517  
 A;Molecule type: protein  
 A;Residues: 1589-1630, 'T', 1722-2058 <GAR3>  
 R;Tresselt, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pan  
 Biochem. J. 274, 731-738, 1991  
 A;Title: Human plasma fibronectin. Demonstration of structural differences between the f  
 A;Reference number: S14357; MUID:91190085; PMID:2012601  
 A;Accession: S14357  
 A;Molecule type: protein  
 A;Residues: 1614-1630, 'T', 1722-2081, 2113-2244 <TRE>  
 R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.  
 J. Biol. Chem. 260, 10320-10325, 1985  
 A;Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-da  
 A;Reference number: A23891; MUID:85261459; PMID:4019516  
 A;Accession: A23891  
 A;Molecule type: protein  
 A;Residues: 2071-2080;2112-2356 <GAR4>  
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 C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,  
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 A;Gene: GDB:FNI  
 A;Cross-references: GDB:119135; OMIM:135600  
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 A;Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1  
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 C;Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplica  
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 F27-31/Domain: propeptide #status predicted <PRO>  
 F32-2386/Product: fibronectin #status experimental <MAT>  
 F52-272/Domain: fibrin and heparin binding <FHB>  
 F52-87/Domain: fibronectin type I repeat homology <1F1>  
 F57-135/Domain: fibronectin type I repeat homology <1F2>  
 F141-179/Domain: fibronectin type I repeat homology <1F3>  
 F186-225/Domain: fibronectin type I repeat homology <1F4>  
 F231-270/Domain: fibronectin type I repeat homology <1F5>  
 F308-608/Domain: collagen binding <CBR>  
 F308-342/Domain: fibronectin type I repeat homology <1F6>  
 F360-401/Domain: fibronectin type II repeat homology <2F1>  
 F420-461/Domain: fibronectin type II repeat homology <2F2>  
 F470-508/Domain: fibronectin type I repeat homology <1F7>  
 F518-555/Domain: fibronectin type I repeat homology <1F8>  
 F561-599/Domain: fibronectin type I repeat homology <1F9>  
 F609-692/Domain: fibronectin type III repeat homology <3FA>  
 F616-706/Domain: heparin binding <HPB>  
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F;1410-1517/Domain: cell attachment <CAD>  
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F;1510-1592/Domain: fibronectin type III repeat homology <FN3K>  
F;1600-1870/Domain: heparin binding <HB2>  
F;1600-1682/Domain: fibronectin type III repeat homology <FN3L>  
F;1692-1773/Domain: fibronectin type III repeat homology <FN3M>  
F;1781-1863/Domain: fibronectin type III repeat homology <FN3N>  
F;1970-1972/Region: cell attachment (R-G-D) motif  
F;1982-2062/Domain: fibronectin type III repeat homology <FN3O>  
F;1985-2216/Domain: fibrin binding <FB2>  
F;2085-2124/Domain: fibronectin type I repeat homology <IF10>  
F;2130-2167/Domain: fibronectin type I repeat homology <IF11>  
F;2174-2209/Domain: fibronectin type I repeat homology <IF12>  
F;1/Modified site: isopropylidene carboxylic acid (Gln) #status experimental  
F;3/Cross-link: isopeptide (Gln) (interchain to Lys N5-amino of fibrin) #status experimental  
F;21-47, 65, 66-94, 92-104, 110-138, 136-148, 155-184, 182-194, 200-229, 227-239, 277-304, 302-313, 315-325, 327-340, 342-353, 355-368, 370-383, 385-398, 399-497, 511, 846, 976, 1213, 1987/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;1205, 1692/Binding site: carbohydrate (Asn) (covalent) #status absent  
F;1943, 1944/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F;2246/Disulfide bonds: interchain (to 2250) #status predicted  
F;2250/Disulfide bonds: interchain (to 2246) #status predicted  
F;2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 71.7%; Score 354; DB 1; Length 2265;  
Best Local Similarity 74.5%; Pred. No. 6.4e-28;  
Matches 70; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDPRLDLEVAATPSTRLLSNRSGLOSRYYRITVYTGEGNSPVQEFVPPWASATIS 60  
Db 1416 VSDPRLDLEVAATPSTRLLSNRSGLOSRYYRITVYTGEGNSPVQEFVPPWASATIS 1475

Qy 61 GLKPGVDYITVYAVTDKSDTYKYDDPISINVRT 94  
Db 1476 GLKPGVDYITVYAVTGRGDSPASSKPFVSINVRT 1509

RESULT 3  
S14428  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049  
R;Hynes, R.O.  
submitted to the EMBL Data Library, July 1989  
A;Reference number: S14428  
A;Accession: S14428  
A;Molecule type: mRNA  
A;Residues: 1-2477 <HYN>  
A;Cross-references: UNIPROT:P04937; EMBL:X15906; NID:G56163; PIDN:CAA34020.1; PID:G561636  
R;Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.  
EMBO J. 6, 2573-2580, 1987  
A;Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.  
A;Reference number: S12455; MUID:88054951; PMID:2445560  
A;Accession: S12455  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 609-1810, 'r', 1812-2283 <SCH>  
A;Cross-references: EMBL:X15906  
R;Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984  
A;Title: A single rat fibronectin gene generates three different mRNAs by alternative splicing.  
A;Reference number: A22319; MUID:84298097; PMID:6089177  
A;Accession: A22319  
A;Molecule type: DNA  
A;Residues: 2052-2237 <TAM>  
R;Falkenberg, C.; Enghild, J.J.; Thøgersen, I.B.; Salvesen, G.; Akerstrøm, B.  
Biochem. J. 301, 745-751, 1994



```

F:2462/Disulfide bonds: interchain (co 2458) #status predicted

Query Match          67.4%; Score 333; DB 2; Length 2477;
Best Local Similarity 68.1%; Pred. No. 1e-25;
Matches 64; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAATPSRLLSWNRSGLQSRYYRITYGETCGNSPVQEFYVPPWASATIS 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1537 VSDVPRDLEVIATPTSLLSISWEPPAVSVRYRITYGETCGNSPVQEFYVPGSKSTATIN 1596
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 GLKPGVDYTTTVAVATDKSDTYKYDDPISINYRT 94
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1597 NIKPGADYTTITVAVTGRGDSPASSRPPVSINYQT 1630
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
A: fibronectin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1998 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A28512
R:Kubomura, S.; Obara, M.; Katasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Hsieh, H.
Biochim. Biophys. Acta 910, 171-181, 1987
A:Title: Genetic analysis of the cell binding domain region of the chicken fibronectin
A:Reference number: A28512; MUID:88050950; PMID:2823899
A:Accession: A28512
A:Molecule type: DNA
A:Residues: 1-273 <KUB>
A:Cross-references: UNIPROT:P11722; GB:X06533; NID:G63393; PIDN:CAA29781.1; PID:
A:Note: the authors translated the codon CCG for residue 190 as Gln, CAG for leu
C:Genetics:
A:Introns: 90/1; 129/1; 184/1; 236/1
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type
C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprote
F:1-82/Domain: fibronectin type III repeat homology (fragment) <FN3I>
F:90-172/Domain: fibronectin type III repeat homology <FN3J>
F:167-169/Region: cell attachment (R-G-D) motif
F:184-266/Domain: fibronectin type III repeat homology <FN3K>

Query Match          63.0%; Score 311; DB 2; Length 273;
Best Local Similarity 64.9%; Pred. No. 1.5e-24;
Matches 61; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAATPSRLLSWNRSGLQSRYYRITYGETCGNSPVQEFYVPPWASATIS 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 90 VSDVPRDLEVNPTSPSLSISWDAPAVTVRYRITYGETGSSPVQEFYVGTMSRATIT 149
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 GLKPGVDYTTTVAVATDKSDTYKYDDPISINYRT 94
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 150 GLKPGVDYTTTVAVTGRGDSPASSRPPVTYTKT 183
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
A29355
A: fibronectin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1998 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29355
R:Norton, P.A.; Hynes, R.O.
Mol. Cell. Biol. 7, 4297-4307, 1987
A:Title: Alternative splicing of chicken fibronectin in embryos and in normal
A:Reference number: A29355; MUID:88142820; PMID:2830487
A:Accession: A29355
A:Molecule type: mRNA
A:Residues: 1-1020 <NOR>
A:Cross-references: UNIPROT:P11722
C:Genetics:
A:Introns: 176/3
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type
C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprote
F:1-86/Domain: fibronectin type III repeat homology <FN3H>
F:92-177/Domain: fibronectin type III repeat homology <FN3I>
F:180-262/Domain: fibronectin type III repeat homology <FN3J>

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A/Accession: A43598  
A/Status: nucleic acid sequence not shown; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-2481 <DES>  
A/Cross-references: GB:M77820  
A/Note: sequence extracted from NCBI backbone (NCBIP:77473)  
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat homology; fibronectin type I repeat homology; glycoprotein; heterodimer  
C/Keywords: duplication; extracellular matrix; repeat homology <1F1>  
F:55-90/Domain: fibronectin type I repeat homology <1F2>  
F:100-138/Domain: fibronectin type I repeat homology <1F3>  
F:144-182/Domain: fibronectin type I repeat homology <1F4>  
F:189-228/Domain: fibronectin type I repeat homology <1F5>  
F:234-273/Domain: fibronectin type I repeat homology <1F6>  
F:309-343/Domain: fibronectin type I repeat homology <1F7>  
F:361-402/Domain: fibronectin type II repeat homology <2F1>  
F:421-462/Domain: fibronectin type II repeat homology <2F2>  
F:471-509/Domain: fibronectin type I repeat homology <1F7>  
F:519-556/Domain: fibronectin type I repeat homology <1F8>  
F:562-600/Domain: fibronectin type I repeat homology <1F9>  
F:610-693/Domain: fibronectin type III repeat homology <FN3A>  
F:719-801/Domain: fibronectin type III repeat homology <FN3B>  
F:810-891/Domain: fibronectin type III repeat homology <FN3C>  
F:906-988/Domain: fibronectin type III repeat homology <FN3D>  
F:996-1077/Domain: fibronectin type III repeat homology <FN3E>  
F:1086-1165/Domain: fibronectin type III repeat homology <FN3F>  
F:1173-1258/Domain: fibronectin type III repeat homology <FN3G>  
F:1266-1349/Domain: fibronectin type III repeat homology <FN3H>  
F:1357-1440/Domain: fibronectin type III repeat homology <FN3I>  
F:1448-1530/Domain: fibronectin type III repeat homology <FN3J>  
F:1538-1620/Domain: fibronectin type III repeat homology <FN3K>  
F:1615-1617/Region: cell attachment (R-G-D) motif  
F:1632-1714/Domain: fibronectin type III repeat homology <FN3L>  
F:1722-1804/Domain: fibronectin type III repeat homology <FN3M>  
F:1812-1894/Domain: fibronectin type III repeat homology <FN3N>  
F:1904-1985/Domain: fibronectin type III repeat homology <FN3O>  
F:1993-2075/Domain: fibronectin type III repeat homology <FN3P>  
F:2197-2277/Domain: fibronectin type III repeat homology <FN3Q>  
F:2301-2340/Domain: fibronectin type I repeat homology <1F10>  
F:2346-2383/Domain: fibronectin type I repeat homology <1F11>  
F:2420-2455/Domain: fibronectin type I repeat homology <1F12>

```

RESULT 8
T42629
tenascin-X - bovine
N:Alternate names: flexilin
C:Species: Bos primigenius taurus (cattle)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42629
R:Eleftheriou, F.; Exposito, J.Y.; Garrone, R.; Lethias, C.
J. Biol. Chem. 272, 22865-22874, 1997
A:Title: Characterization of the bovine tenascin-X.
A:Reference number: Z221180; MUID:97426436; PMID:9278449
A:Accession: T42629
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4135 <LE>
A:Cross-references: UNIPROT:O18977; EMBL:Y11915; NID:G2462978; PIDN:CAA7267

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A;Residues: 1-4135 <ELE>  
A;Cross-references: UNIPROT:O18977; EMBL:Y11915; NID:G2462978; PIDN:CAA72671.1; PID:G246

C/Genetics:  
A/Gene: TN-X  
C/Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type  
C/Keywords: extracellular matrix; glycoprotein; heptad repeat

Query Match 25.1%; Score 124; DB 2; Length 4135;  
Best Local Similarity 35.9%; Pred. No. 0.0006;  
Matches 33; Conservative 17; Mismatches 36; Indels 6; Gaps 3;

QY 3 DVPRDLVVAATPTSLRSLGNRSGLQSRYYRTYGTGNSPVQERTVPPWASIIATISGL 62  
DB 840 DGEQDURVAVPTTLELNLRLPQAEVDPRVSVY-VSAGNQVR-LEVPSEADGILLTGL 897  
QY 63 KPGVDYITVYATDKSDTYKDDPISINVRT 94  
DB 898 MEGVEIVVITAEGRVAVY----PASIRANT 925

RESULT 9  
JH0675  
restrictin precursor - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: JH0675; PS0385; S23254  
R/Noerenberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, F.G.  
Neuron 8, 849-863, 1992  
A/Title: The chicken neural extracellular matrix molecule restrictin: similarity with EG  
A/Reference number: JH0675; MUID:92265298; PMID:1375037  
A/Accession: JH0675  
A/Molecule type: mRNA  
A/Residues: 1-1353 <NOB>  
A/Cross-references: UNIPROT:Q00546; GB:X64649; NID:G63613; PIDN:CAA45920.1; PID:G63614  
A/Experimental source: brain  
A/Accession: PS0385  
A/Molecule type: protein  
A/Residues: 579-586;827-840 <NOE1>  
A/Comment: This protein is a neural extracellular matrix protein implicated in neural ce  
C/Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin typ  
C/Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycoprot  
F,1-33/Domain: signal sequence #status predicted <SIG>  
F,34-1353/Product: restrictin #status predicted <MAT>  
F,203-229/Domain: EGF homology <EG1>  
F,234-260/Domain: EGF homology <EG2>  
F,265-291/Domain: EGF homology <EG3>  
F,296-322/Domain: EGF homology <EG4>  
F,324-405/Domain: fibronectin type III repeat homology <FN1>  
F,413-494/Domain: fibronectin type III repeat homology <FN2>  
F,502-584/Domain: fibronectin type III repeat homology <FN3>  
F,592-676/Domain: fibronectin type III repeat homology <FN4>  
F,684-764/Domain: fibronectin type III repeat homology <FN5>  
F,772-853/Domain: fibronectin type III repeat homology <FN6>  
F,861-941/Domain: fibronectin type III repeat homology <FN7>  
F,949-1027/Domain: fibronectin type III repeat homology <FN8>  
F,1035-1115/Domain: fibronectin type III repeat homology <FN9>  
F,1130-1338/Domain: fibronectin type III repeat homology <FN9>  
F,1272-1286/Region: calcium binding #status predicted  
F,53,197,277,391,469,580,734,790,960,1031,1041,1256,1342/Binding site: carbohydrate (Asn  
F,53,197,277,391,469,580,734,790,960,1031,1041,1256,1342/Binding site: carbohydrate (Asn

Query Match 24.5%; Score 121; DB 1; Length 1353;  
Best Local Similarity 40.3%; Pred. No. 0.00034;  
Matches 29; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 3 DVPRDLVVAATPTSLRSLGNRSGLQSRYYRTYGTGNSPVQERTVPPWASIIATISGL 62  
DB 686 DSPRDLVLTASTETISLSLTKAMGPIDHYRVTF--TPASGMASEVTVGRNESQLTSL 743  
QY 63 KPGVDYITVY 74  
DB 744 EPGTETITIIA 755

RESULT 10  
S19694

tenascin precursor - pig  
N/Alternate names: contactin; hexabrachion  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: S19694  
R/Nishi, T.; Weinstein, J.; Gillespie, W.M.; Paulson, J.C.  
Eur. J. Biochem. 202, 643-648, 1991  
A/Title: Complete primary structure of porcine tenascin. Detection of tenascin transcrip  
A/Reference number: S19694; MUID:92104189; PMID:1722152  
A/Accession: S19694  
A/Molecule type: mRNA  
A/Residues: 1-1746 <NIS>  
A/Cross-references: UNIPROT:Q29116; EMBL:X61599; NID:G2124; PIDN:CAA43796.1; PID:G2125  
C/Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type  
C/Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell  
F,1-22/Domain: signal sequence #status predicted <SIG>  
F,23-1746/Product: tenascin #status predicted <MAT>  
F,346-372/Domain: EGF homology <EGF>  
F,377-403/Domain: EGF homology <EGF2>  
F,622-703/Domain: fibronectin type III repeat homology <FN3A>  
F,711-793/Domain: fibronectin type III repeat homology <FN3B>  
F,802-884/Domain: fibronectin type III repeat homology <FN3C>  
F,892-976/Domain: fibronectin type III repeat homology <FN3D>  
F,984-1084/Domain: fibronectin type III repeat homology <FN3E>  
F,1073-1155/Domain: fibronectin type III repeat homology <FN3F>  
F,1164-1246/Domain: fibronectin type III repeat homology <FN3G>  
F,1254-1335/Domain: fibronectin type III repeat homology <FN3H>  
F,1343-1423/Domain: fibronectin type III repeat homology <FN3I>  
F,1431-1511/Domain: fibronectin type III repeat homology <FN3J>  
F,1526-1734/Domain: fibronectin type III repeat homology <FN3K>  
F,38,166,184,327,788,1034,1079,1121,1354/Binding site: carbohydrate (Asn) (covalent) #st  
Query Match 24.5%; Score 121; DB 1; Length 1746;  
Best Local Similarity 35.1%; Pred. No. 0.00045;  
Matches 33; Conservative 14; Mismatches 41; Indels 6; Gaps 3;

QY 3 DVPRDLVVAATPTSLRSLGNRSGLQSRYYRTYGTG--NSPVQERTVPPWASIIATIS 60  
DB 894 DAPRNLRLISQTDNSITLEWRNGKAAADYRIKYAPISGGDHAEVEVPRSPQTTTKATLT 953  
QY 61 GLKPGVDYITVYATDKSDTYKDDPISINVRT 94  
DB 954 GLRPGTEYGIGVSAV--RGD--KESDPATINAAT 983

RESULT 11  
A45445  
janusin precursor, long form - rat  
N/Alternate names: neural recognition glycoprotein J1-160/180, long form  
N/Contains: neural recognition glycoprotein J1-160/180, short form  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C/Accession: A45445; B45445; S32023  
R/Fuss, B.; Wintergerst, E.S.; Bartsch, U.; Schachner, M.  
J. Cell Biol. 120, 1237-1249, 1993  
A/Title: Molecular characterization and in situ mRNA localization of the neural recognit  
A/Reference number: A45445; MUID:93171267; PMID:7679676  
A/Accession: A45445  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-1356 <FUS>  
A/Cross-references: UNIPROT:Q05546; GB:Z18630; NID:G57961; PIDN:CAA79229.1; PID:G57962  
A/Accession: B45445  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-772,863-1356 <FU2>  
A/Cross-references: GB:Z18630  
R/Fuss, B.; Wintergerst, E.; Bartsch, U.; Schachner, M.  
submitted to the EMBL Data Library, November 1992  
A/Description: Molecular characterization and in situ mRNA localization of the neural re  
A/Reference number: S32023  
A/Accession: S32023  
A/Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-1356 <FUS2>  
A:Cross-references: EMBL:Z18630; NID:G57961; PIDN:CAA79229.1; PID:G57962  
C:Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; glycoprotein  
C:Keywords: alternative splicing; duplication; fibrinogen beta/gamma homology; glycoprotein; oligo  
F:1-1356/Product: janusin, long form #status experimental <MAT>  
F:1-172,863-1356/Product: janusin, short form #status experimental <ALT>  
F:204-230/Domain: EGF homology <EG1>  
F:235-261/Domain: EGF homology <EG2>  
F:266-292/Domain: EGF homology <EG3>  
F:297-323/Domain: EGF homology <EG4>  
F:325-405/Domain: fibrinectin type III repeat homology <FN1>  
F:413-494/Domain: fibrinectin type III repeat homology <FN2>  
F:502-594/Domain: fibrinectin type III repeat homology <FN3>  
F:592-676/Domain: fibrinectin type III repeat homology <FN4>  
F:684-764/Domain: fibrinectin type III repeat homology <FN5>  
F:772-854/Domain: fibrinectin type III repeat homology <FN6>  
F:1038-1118/Domain: fibrinectin type III repeat homology <FN7>  
F:1133-1341/Domain: fibrinogen beta/gamma homology <FBG>  
  
Query Match 23.5%; Score 116; DB 2; Length 1356;  
Best Local Similarity 27.4%; Pred. No. 0.0011;  
Matches 34; Conservative 18; Mismatches 36; Indels 36; Gaps 3;  
  
Qy 3 DVPRDLVVAATPTSRLLSWNSGLQSYRYITVGTGNSPVQSFVTPVPWASITATISGL 62  
Db 686 DSPRDLVMTASSETSLIWTKASGPDIDYRITETPPSGIS--SEVTVPDRDTSYTLTDL 743  
  
Qy 63 KPGVDYITITVA-----VTDKSDTYKYDDP-----I 88  
Db 744 EPGAIIISITAEGRQOSLESTVDATFGFRPISHLHFSHTSSVNTWSDSPPPADRL 803  
  
Qy 89 SINY 92  
Db 804 ILNY 807  
  
RESULT 12  
A40701  
tenascin-X precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A40701; A33725; C42175  
R:Bristow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.  
J. Cell Biol. 122, 265-278, 1993  
A:Title: Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene c  
A:Reference number: A40701; MUID:93300909; PMID:7686164  
A:Accession: A40701  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-3566 <BRI>  
A:Cross-references: UNIPROT:P22105; UNIPROT:Q9UC11; EMBL:X71937  
R:Morel, Y.; Bristow, J.; Gitelman, S.E.; Miller, W.L.  
Proc. Natl. Acad. Sci. U.S.A. 86, 6582-6586, 1989  
A:Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/c  
A:Reference number: A33725; MUID:89367293; PMID:2475872  
A:Accession: A33725  
A:Molecule type: mRNA  
A:Residues: 2748-3199, 'V', 3201-3298, 'E', 3299-3314, 'G', 3316-3566 <MOR>  
A:Cross-references: GB:M25813; NID:G183069; PIDN:AAA35884.1; PID:G183070  
R:Matsumoto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.  
Genomics 12, 485-491, 1992  
A:Title: Cluster of fibrinectin type III repeats found in the human major histocompatibi  
enascin.  
A:Reference number: A42175; MUID:92217969; PMID:1373119  
A:Accession: C42175  
A:Molecule type: DNA  
A:Residues: 1849-1936 <MAT>  
A:Experimental source: clone 3.9kF3-1  
A:Note: sequence extracted from NCI backbone (NCBIP:95694)  
C:Genetics:  
A:Gene: GDB:TNXA; D6S103E; TNX; XA; XB  
A:Cross-references: GDB:568487; OMIM:600261

A:Map position: 6p21.3-6p21.3  
C:Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibrinectin typ  
C:Keywords: extracellular matrix; glycoprotein  
F:748-828/Domain: fibrinectin type III repeat homology <3F1>  
F:829-856/Domain: fibrinectin type III repeat homology #status atypical <3F2>  
F:873-953/Domain: fibrinectin type III repeat homology <3F3>  
F:975-1055/Domain: fibrinectin type III repeat homology <3F4>  
F:1167-1247/Domain: fibrinectin type III repeat homology <3F5>  
F:1248-1317/Domain: fibrinectin type III repeat homology #status atypical <3F7>  
F:1323-1403/Domain: fibrinectin type III repeat homology <3F8>  
F:1412-1492/Domain: fibrinectin type III repeat homology <3F9>  
F:1510-1590/Domain: fibrinectin type III repeat homology #status atypical <3F10>  
F:1618-1676/Domain: fibrinectin type III repeat homology <3F11>  
F:1678-1749/Domain: fibrinectin type III repeat homology #status atypical <3F12>  
F:1751-1831/Domain: fibrinectin type III repeat homology <3F13>  
F:1849-1929/Domain: fibrinectin type III repeat homology <3F14>  
F:1955-2035/Domain: fibrinectin type III repeat homology <3F15>  
F:2061-2141/Domain: fibrinectin type III repeat homology <3F16>  
F:2167-2246/Domain: fibrinectin type III repeat homology <3F17>  
F:2274-2354/Domain: fibrinectin type III repeat homology <3F18>  
F:2382-2462/Domain: fibrinectin type III repeat homology <3F19>  
F:2488-2568/Domain: fibrinectin type III repeat homology <3F20>  
F:2584-2664/Domain: fibrinectin type III repeat homology <3F21>  
F:2677-2757/Domain: fibrinectin type III repeat homology <3F22>  
F:2771-2851/Domain: fibrinectin type III repeat homology <3F23>  
F:2878-2958/Domain: fibrinectin type III repeat homology <3F24>  
F:2977-3067/Domain: fibrinectin type III repeat homology #status atypical <3F25>  
F:3078-3159/Domain: fibrinectin type III repeat homology <3F26>  
F:3167-3247/Domain: fibrinectin type III repeat homology <3F27>  
F:3255-3334/Domain: fibrinectin type III repeat homology <3F28>  
F:3349-3557/Domain: fibrinogen beta/gamma homology <FBG>  
  
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Best Local Similarity 31.9%; Pred. No. 0.011;  
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Db 748 VIDGPDRLVVSVTPTTLEGLRLPQAEVDFVSVY-VSADNQVR-LEVPPETDGTLLT 805  
  
Qy 61 GLKPGVDYITITVAVTDKSDTYKYDDPISINRYT 94  
Db 806 DLMPGVEYVTVTAERGRAVSY---PASVRANT 835  
  
RESULT 13  
S46216  
leukocyte antigen-related protein precursor - rat  
N:Alternate names: leukocyte common antigen homology  
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S46216; S23252; A41032; A33154  
R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
Biochem. J. 302, 39-47, 1994  
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho  
A:Reference number: S46216; MUID:94347119; PMID:8068021  
A:Accession: S46216  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1898 <ZHA>  
A:Cross-references: UNIPROT:Q64604; EMBL:L11586; NID:G205132; PIDN:AAC37655.1; PID:G2051  
R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.  
Biochem. J. 284, 569-576, 1992  
A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by thre  
A:Reference number: S23126; MUID:92287069; PMID:1599438  
A:Accession: S23126  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1361-1604; 1649-1898 <HAS>  
R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.



R;Jones, F.S.; Burgoon, M.P.; Hoffman, S.; Crossin, K.L.; Cunningham, B.A.; Edelman, G.M.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 2186-2190, 1988  
 A;Title: A cDNA clone for cytotoxicin contains sequences similar to epidermal growth factor  
 A;Reference number: A31930; MUID:88176910; PMID:2451243  
 A;Accession: A31930  
 A;Molecule type: mRNA  
 A;Residues: 1-933 <JON>  
 A;Cross-references: UNIPROT:P10039  
 A;Note: the authors' translation of the codons for residues 601-620 differs considerably  
 C;Superfamily: tenascin; EGF homology; fibronogen beta/gamma homology; fibronectin type  
 C;Keywords: alternative splicing; glycoprotein  
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 F;223-307/Domain: fibronectin type III repeat homology <FN3B>  
 F;315-399/Domain: fibronectin type III repeat homology <FN3C>  
 F;407-491/Domain: fibronectin type III repeat homology <FN3D>  
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 F;587-668/Domain: fibronectin type III repeat homology <FN3F>  
 F;765-845/Domain: fibronectin type III repeat homology <FN3G>  
 F;860-933/Domain: fibronogen beta/gamma homology (fragment) <FBG>  
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 Best Local Similarity 33.7%; Pred. No. 0.0048;  
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 Db 409 DAPNLRKVSQTDNSITLWKFSHANIDNYRIKAPISGGDHT-ELTVPKGNQATTRATL 467  
 Qy 60 SGLKPGVDYTTTVYAVTDKSDTYKYDDPISINYRT 94  
 Db 468 TGLRPGTEYGIGVTAVRODRES---APATINAGT 498

Search completed: May 18, 2005, 15:47:44  
 Job time : 41 secs

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4	361	73.1	2240	2	Q68DP8	Q68dp8 homo sapien
5	361	73.1	2267	2	Q68DP9	Q68dp9 homo sapien
6	361	73.1	2296	2	Q6N0A6	Q6nta6 homo sapien
7	361	73.1	2257	2	Q68DT4	Q68dt4 homo sapien
8	361	73.1	2386	1	FINC HUMAN	P02751 homo sapien
9	361	73.1	2444	2	Q6N0Z5	P06025 homo sapien
10	361	73.1	2477	2	Q6MZU5	Q6mzu5 homo sapien
11	356	72.1	2193	2	Q6MZM7	Q6mzm7 homo sapien
12	354	71.7	2265	1	FINC BOVIN	P07589 bos taurus
13	333	67.4	2477	1	FINC MOUSE	P11276 mus musculus
14	333	67.4	2477	1	FINC RAT	P04937 rattus norv
15	311	63.0	1256	1	FINC CHICK	P11722 gallus gall
16	269	54.5	293	2	Q9XSG0	Q9xsg0 cryptolagus
17	264	53.4	1328	1	FINC PLEWA	Q91289 pteryodotes
18	262	53.0	2481	1	FINC XENLA	Q91740 xenopus lae
19	262	53.0	2481	2	Q6QQA5	Q6qqa5 xenopus lae
20	251	50.8	2478	2	Q93406	Q93406 brachydanio
21	246	49.8	2408	2	Q6JAN2	Q6jan2 brachydanio
22	153	31.0	68	2	Q28692	Q28692 cryptolagus
23	130	26.3	522	1	FINC HORSE	Q28377 equus caball
24	125	25.3	4006	2	O35452	Q35452 mus musculus
25	125	25.3	4114	2	O54796	O54796 mus musculus
26	124	25.1	4135	2	O18977	O18977 bos taurus
27	123	24.9	320	2	Q95KV4	Q95kv4 bos taurus
28	123	24.9	347	2	Q95KV5	Q95kv5 bos taurus
29	123	24.9	426	2	Q9NPK8	Q9npk8 homo sapien
30	123	24.9	522	1	FINC CANFA	Q28275 canis famil
31	123	24.9	1350	2	Q773T6	Q7t336 brachydanio



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 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_2.  
 DR PROSITE; PS01253; FIBRONECTIN\_1; 10.  
 DR PROSITE; PS00023; FIBRONECTIN\_2; 2.  
 KW Hypothetical protein.  
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Query Match 73.1%; Score 361; DB 2; Length 2240;  
 Best Local Similarity 77.7%; Pred. No. 2e-29;  
 Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

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 Db 1447 VSDVPRDLEVVAAPTSLISWNPAPVTVVYRITYGETGNSPVQSEFTVPGSKSTATIS 1506

Qy 61 GLKPGVDYTTIVVAVTOKSDTYKYDDPISINVRT 94  
 Db 1507 GLKPGVDYTTIVVAVTGRGDSPASSKPIISINVRT 1540

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 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DE Hypothetical protein DKFZp686K08164.  
 GN Name=DKFZp686K08164;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus endothel;  
 RG The German cDNA Consortium;  
 RA Koeber K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR749316; CAH18171.1; -.  
 DR InterPro; IPR002086; Aldehyde dehydrog.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR000083; Fibrinctn1.  
 DR InterPro; IPR003962; FNIII subd.  
 DR InterPro; IPR003961; FNIII-like.  
 DR InterPro; IPR008957; FNIII-like.  
 DR Pfam; PF00039; fn1; 12.  
 DR Pfam; PF00040; fn2; 2.  
 DR Pfam; PF00041; fn3; 16.  
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 DR PRINTS; PR00013; FNTYPEII.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR ProDom; PD000995; FN\_Type\_II; 2.  
 DR SMART; SM00058; FN1; 12.  
 DR SMART; SM00059; FN2; 2.  
 DR SMART; SM00060; FN3; 16.  
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 DR PROSITE; PS01253; FIBRONECTIN\_1; 12.  
 DR PROSITE; PS00023; FIBRONECTIN\_2; 2.  
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Query Match 73.1%; Score 361; DB 2; Length 2267;  
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Qy 1 VSDVPRDLEVVAAPTSLISWNRSGLSQSRYYRITYGETGNSPVQSEFTVPPWASIIATIS 60  
 Db 1538 VSDVPRDLEVVAAPTSLISWNPAPVTVVYRITYGETGNSPVQSEFTVPGSKSTATIS 1597

Qy 61 GLKPGVDYTTIVVAVTOKSDTYKYDDPISINVRT 94  
 Db 1598 GLKPGVDYTTIVVAVTGRGDSPASSKPIISINVRT 1631

RESULT 6  
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 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein DKFZp686M04163.  
 GN Name=DKFZp686M04163;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human uterus cDNA Consortium;  
 RG The German Human cDNA Consortium;  
 RA Bloeker H., Boescher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640608; CAB45714.1; -.  
 DR GO; GO:000576; C:extracellular; IEA.  
 DR InterPro; IPR02086; Aldehyde dehydrog.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR000083; Fibrinctn1.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR000562; FN\_Type\_II.  
 DR Pfam; PF00039; fn1; 12.  
 DR Pfam; PF00040; fn2; 2.  
 DR Pfam; PF00041; fn3; 15.  
 DR PRINTS; PR00012; FNTYPEI.  
 DR PRINTS; PR00013; FNTYPEII.  
 DR ProDom; PD000995; FN\_Type\_II; 2.  
 DR SMART; SM00058; FN1; 12.  
 DR SMART; SM00059; FN2; 2.  
 DR SMART; SM00060; FN3; 15.  
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 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_2.  
 DR PROSITE; PS01253; FIBRONECTIN\_1; 12.  
 DR PROSITE; PS00023; FIBRONECTIN\_2; 2.  
 DR PROSITE; PS00853; FN3; 15.  
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 Db 1447 VSDVPRDLEVVAAPTSLISWNPAPVTVVYRITYGETGNSPVQSEFTVPGSKSTATIS 1506

Qy 61 GLKPGVDYTTIVVAVTOKSDTYKYDDPISINVRT 94  
 Db 1507 GLKPGVDYTTIVVAVTGRGDSPASSKPIISINVRT 1540

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 AC Q68DT4;  
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 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DE Hypothetical protein DKFZp686F10164.  
 GN Name=DKFZp686F10164;  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN NCBI\_TaxID=9606;  
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 RN SEQUENCE FROM N.A.  
 RC TISSUE=Uterus endothel;  
 RG The German cDNA Consortium;  
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RL Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR749281; CAH18136.1; -  
 DR InterPro; IPR002086; Aldehyd dehydrog.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR000083; Fibrinctnl.  
 DR InterPro; IPR003962; FnIII subd.  
 DR InterPro; IPR003961; Fn\_III.  
 DR InterPro; IPR008957; Fn\_III-like.  
 DR InterPro; IPR000562; FN\_Type\_II.  
 DR Pfam; PF000039; fn1; 12.  
 DR Pfam; PF00040; fn2; 2.  
 DR Pfam; PF00041; fn3; 15.  
 DR PRINTS; PR00012; FNTYPEI.  
 DR PRINTS; PR00013; FNTYPEII.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR ProDom; PD000208; FN\_Type\_II; 2.  
 DR SMART; SM00058; FN1; 12.  
 DR SMART; SM00059; FN2; 2.  
 DR SMART; SM00060; FN3; 15.  
 DR PROSITE; PS00687; ALDEHYDE DEHYDR\_GLU; UNKNOWN\_1.  
 DR PROSITE; PS0022; EGF 1; UNKNOWN\_2.  
 DR PROSITE; PS01253; FIBRONECTIN\_1; 12.  
 DR PROSITE; PS00023; FIBRONECTIN\_2; 2.  
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 SQ SEQUENCE 2357 AA; 259090 MW; BEAE3990E27E532A CRC64;  
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 Best Local Similarity 77.7%; Pred. No. 2.1e-29;  
 Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 VSDVPRDLVVAATPTSLISNNRSLGQSYRYRITYGTGGNSPVQEFVTPGSKSTATIS 60  
 DB 1539 VSDVPRDLVVAATPTSLISNNRSLGQSYRYRITYGTGGNSPVQEFVTPGSKSTATIS 1598  
 QY 61 GLKPGVDYITVYAVTGDYKYDDPISINYET 94  
 DB 1599 GLKPGVDYITVYAVTGRGDSPASSRKPISINYET 1632  
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 AC P02751; O95609; O95610; Q14312; Q14325; Q14326; Q86T27; Q8IV18;  
 AC Q96KP7; Q96KP8; Q96KP9; Q9H1B8; Q9HAP3; Q9UMK2;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).  
 GN Name=FN1; Synonyms=FN;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RA MEDLINE=21600194; PubMed=11737888; DOI=10.1186/bcr325;  
 RA Schor S.L., Schor A.M.;  
 RT "Phenotypic and genetic alterations in mammary stroma: implications  
 RT for tumour progression";  
 RL Breast Cancer Res. 3:373-379(2001).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORMS 3; 7 AND 10).  
 RC TISSUE=Cervix;  
 RA Ansoorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,

RA Mewes H.-W., Weil B., Amid C., Osanger A., Fobo G., Han M.,  
 RA Wiemann S.;  
 RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE OF 1-38 FROM N.A.  
 RP MEDLINE=87030890; PubMed=3770189; DOI=10.1016/0014-5793(86)80029-1;  
 RA Gutman A., Yamada K.M., Kornblitt A.R.;  
 RT "Human fibronectin is synthesized as a pre-propolypeptide";  
 RL FEBS Lett. 207:145-148(1986).  
 RN [4]  
 RN SEQUENCE OF 1-49 FROM N.A.  
 RP MEDLINE=87175578; PubMed=3031656;  
 RA Dean D.C., Bowlus C.L., Bourgeois S.;  
 RT "Cloning and analysis of the promotor region of the human fibronectin  
 RT gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).  
 RN [5]  
 RN SEQUENCE OF 28-2386 FROM N.A. (ISOFORM 3).  
 RP MEDLINE=85284965; PubMed=2992939;  
 RA Kornblitt A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;  
 RT "Primary structure of human fibronectin: differential splicing may  
 RT generate at least 10 polypeptides from a single gene.";  
 RL EMBO J. 4:1755-1759(1985).  
 RN [6]  
 RN SEQUENCE OF 103-481 AND 2228-2386 FROM N.A. (ISOFORMS 1; 3; 8 AND 9).  
 RC TISSUE=Peripheral blood T-cell, and Umbilical vein endothelial cells;  
 RA Godfrey H.P., Ebrahim A.A.;  
 RT Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RL [7]  
 RN SEQUENCE OF 973-2386 FROM N.A. (ISOFORM 3).  
 RP MEDLINE=84272258; PubMed=6462919;  
 RA Kornblitt A.R., Vibe-Pedersen K., Baralle F.E.;  
 RT "Human fibronectin: cell specific alternative mRNA splicing generates  
 RT polypeptide chains differing in the number of internal repeats";  
 RL Nucleic Acids Res. 12:5853-5868(1984).  
 RN [8]  
 RN SEQUENCE OF 1232-1782 FROM N.A. (ISOFORM 7).  
 RP MEDLINE=88233940; PubMed=3375063;  
 RA Paolella G., Henschliffe C., Sebastio G., Baralle F.E.;  
 RT "Sequence analysis and in vivo expression show that alternative  
 RT splicing of ED-B and ED-A regions of the human fibronectin gene are  
 RT independent events";  
 RL Nucleic Acids Res. 16:3545-3557(1988).  
 RN [9]  
 RN SEQUENCE OF 1257-1365 FROM N.A. (ISOFORM 11).  
 RP MEDLINE=88041070; PubMed=3478690;  
 RA Gutman A., Kornblitt A.R.;  
 RT "Identification of a third region of cell-specific alternative  
 RT splicing in human fibronectin mRNA";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7179-7182(1987).  
 RN [10]  
 RN SEQUENCE OF 1441-1548.  
 RP MEDLINE=82265604; PubMed=7050098;  
 RA Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;  
 RT "The cell attachment domain of fibronectin. Determination of the  
 RT primary structure";  
 RL J. Biol. Chem. 257:9593-9597(1982).  
 RN [11]  
 RN SEQUENCE OF 1448-1540 FROM N.A.  
 RP MEDLINE=83290929; PubMed=6688418;  
 RA Oldberg A., Linney E., Ruoslahti E.;  
 RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for  
 RT the cell attachment domain in human fibronectin";  
 RL J. Biol. Chem. 258:10193-10196(1983).  
 RN [12]  
 RN SEQUENCE OF 1448-1540 FROM N.A.  
 RP MEDLINE=86111901; PubMed=3003095;  
 RA Oldberg A., Ruoslahti E.;  
 RT "Evolution of the fibronectin gene. Exon structure of cell attachment  
 RT domain";  
 RL J. Biol. Chem. 261:2113-2116(1986).  
 RN [13]  
 RN SEQUENCE OF 1594-2386 FROM N.A. (ISOFORM 1).

EX MEDLINE=85280409; PubMed=2992573;  
RA "Bernard M.P., Kolbe W., Weil D., Chu M.-L.;  
RT Human cellular fibronectin: comparison of the carboxyl-terminal  
RT portion with rat identifies primary structural domains separated by  
RT hypervariable regions.";  
RL Biochemistry 24:2698-2704 (1985).  
RN [14]  
RP SEQUENCE OF 1712-1739 FROM N.A.  
RX MEDLINE=87026578; PubMed=3021206;  
RA Sekiguchi K., Klos A.M., Kurachi K., Yoshitake S., Hakomori S.;  
RT "Human liver fibronectin complementary DNAs: identification of two  
RT different messenger RNAs possibly encoding the alpha and beta subunits  
RT of plasma fibronectin.";  
RL Biochemistry 25:4936-4941 (1986).  
RN [15]  
RP SEQUENCE OF 1788-2386 FROM N.A. (ISOFORMS 4; 5 AND 6).  
RC TISSUE=Cartilage;  
RX MEDLINE=22126816; PubMed=12127832; DOI=10.1053/joca.2002.0792;  
RA Parker A.E., Boutell J., Carr A., Maciewicz R.A.;  
RT "Novel cartilage-specific splice variants of fibronectin.";  
RL Osteoarthritis Cartilage 10:528-534 (2002).  
RN [16]  
RP SEQUENCE OF 32-290.  
RX MEDLINE=84032463; PubMed=6630202;  
RA Garcia-Pardo A., Pearlstein E., Frangione B.;  
RT "Primary structure of human plasma fibronectin. The 29,000-dalton NH2-  
RT terminal domain.";  
RL J. Biol. Chem. 258:12670-12674 (1983).  
RN [17]  
RP SEQUENCE OF 109-608, AND COLLAGEN-BINDING.  
RX MEDLINE=87080265; PubMed=3024962;  
RA Owens R.J., Baralle F.E.;  
RT "Mapping the collagen-binding site of human fibronectin by expression  
RT in *Escherichia coli*.";  
RL EMBO J. 5:2825-2830 (1986).  
RN [18]  
RP SULFATION.  
RX MEDLINE=86042625; PubMed=2414772;  
RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;  
RT "Tyrosine sulfation of proteins from the human hepatoma cell line  
RT HepG2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164 (1985).  
RN [19]  
RP O-GLYCOSYLATION OF THR-2064.  
RX MEDLINE=91190085; PubMed=2012601;  
RA Tressel T., McCarthy J.B., Calaycay J., Lee T.D., Legesse K.,  
RA Shively J.E., Pande H.;  
RT "Human plasma fibronectin. Demonstration of structural differences  
RT between the A- and B-chains in the III CS region.";  
RL Biochem. J. 274:731-738 (1991).  
RN [20]  
RP FBN1-BINDING SITE.  
RX MEDLINE=93015879; PubMed=1400330;  
RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,  
RA Argraves W.S.;  
RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding  
RT region of fibronectin.";  
RL J. Biol. Chem. 267:20120-20125 (1992).  
RN [21]  
RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.  
RX MEDLINE=95081153; PubMed=7989369;  
RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;  
RT "Further characterization of the NH2-terminal fibrin-binding site on  
RT fibronectin.";  
RL J. Biol. Chem. 269:31938-31945 (1994).  
RN [22]  
RP INTERACTION WITH LGALS3BP.  
RX PubMed=9501082; DOI=10.1093/emboj/17.6.1606;  
RA Sakaki T., Brakebusch C., Engel J., Timpl R.;  
RT "Mac-2 binding protein is a cell-adhesive protein of the extracellular  
RT matrix which self-assembles into ring-like structures and binds beta1  
RT integrins, collagens and fibronectin.";  
RL EMBO J. 17:1606-1613 (1998).

[23]  
RN STRUCTURE BY NMR OF 1447-1540.  
RX MEDLINE=92162710; PubMed=1311202;  
RA Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,  
RA Campbell I.D.;  
RT "1H NMR assignment and secondary structure of the cell adhesion type  
RT III module of fibronectin.";  
RL Biochemistry 31:2068-2073 (1992).  
RN [24]  
RP STRUCTURE BY NMR OF 1447-1540.  
RX MEDLINE=93046665; PubMed=1423622; DOI=10.1016/0092-8674(92)90600-H;  
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;  
RT "The three-dimensional structure of the tenth type III module of  
RT fibronectin: an insight into RGD-mediated interactions.";  
RL Cell 71:671-678 (1992).  
RN [25]  
RP STRUCTURE BY NMR OF 182-275.  
RX MEDLINE=94141923; PubMed=8308892;  
RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,  
RA Campbell I.D.;  
RT "Solution structure of a pair of fibronectin type I modules with  
RT fibrin binding activity.";  
RL J. Mol. Biol. 235:1302-1311 (1994).  
RN [26]  
RP STRUCTURE BY NMR OF 32-92.  
RX MEDLINE=96069779; PubMed=7583666;  
RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;  
RT "High-resolution structural studies of the factor XIIIa crosslinking  
RT site and the first type I module of fibronectin.";  
RL Nat. Struct. Biol. 2:946-950 (1995).  
RN [27]  
Query Match 73.1%; Score 361; DB 1; Length 2386;  
Best Local Similarity 77.7%; Pred. No. 2.1e-29;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
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Db 1447 VSDVPRDLEVAATPTSRLLISWNRSGLQSYRYRYTYGTGNSPVQSFVTPPWASIAIS 1506  
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Db 1507 GLKPGVDYTTTVAVTQKSDPTKYDDPISINRYT 1540  
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AC Q6N025;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686M2451 (Fragment).  
GN Name=DKFZp686M2451;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A.  
RC TISSUE=Human endometrium carcinoma cell line;  
RG The German Human cDNA Consortium;  
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640731; CA645847.1;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR InterPro; IPR02086; Aldehyd dehydrog.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR000083; Fibrinctnl.  
DR InterPro; IPR003961; FN\_III-like.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR00562; FN\_Type\_II.

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DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 16.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 16.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00222; EGF 1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 16.
KW Hypothetical protein.
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Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

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Db 1536 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYTGSGNSPVQSEFTVPWGSKSTATIS 1595

QY 61 GLKPGVDYITTVAVYATKSDTYKYDDPISINVRT 94
Db 1596 GLKPGVDYITTVAVYATGRGDSPASSKPIISINVRT 1629

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Human endometrium carcinoma cell line;
RG The German Human CDNA Consortium;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640875; CAE45932.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 7.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00013; FNTYPEI.
DR PRINTS; PR00014; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 7.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 17.
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DR PROSITE; PS00222; EGF 1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 17.
KW Hypothetical protein.
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Best Local Similarity 77.7%; Pred. No. 2.2e-29;
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QY 61 GLKPGVDYITTVAVYATKSDTYKYDDPISINVRT 94
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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GN Name=DKFZp686O12165;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Human uterine endothel primary cell culture;
RG The German Human CDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640099; CAE46002.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 7.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 7.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 17.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00222; EGF 1; UNKNOWN_1.
DR PROSITE; PS01253; FIBRONECTIN_1; 7.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 17.
KW Hypothetical protein.
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QY 61 GLKPGVDYITTVAVYATKSDTYKYDDPISINVRT 94
Db 1345 GLKPGVDYITTVAVYATGRGDSPASSKPIISINVRT 1378

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RESULT 12
ID_FINC_BOVIN STANDARD; PRT; 2265 AA.
AC P07589.
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibronection (FN).
GN Name=FN1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RX MEDLINE=87054047; PubMed=3780752;
RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin.";
RL Eur. J. Biochem. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=83117805; PubMed=6218503;
RA Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
RA Sahl P., Sottrup-Jensen L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
of internal homology.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
RN [3]
RX MEDLINE=83221567; PubMed=6304699;
RA Kornblitt A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
fibronectins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
CC -!- FUNCTION: Fibronectins bind cell surfaces and various compounds
including collagen, fibrin, heparin, DNA, and actin. Fibronectins
are involved in cell adhesion, cell motility, opsonization, wound
healing, and maintenance of cell shape.
CC -!- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
variants, connected by 2 disulfide bonds near the carboxyl ends;
to a lesser extent homodimers.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced. Each of the "extra
domain" and the connecting strand 3 are present in some forms of
fibronectin and absent in others;
Name=1;
CC -!- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
forms), made by fibroblasts, epithelial and other cell types, is
deposited as fibrils in the extracellular matrix.
CC -!- PTM: Sulfated (By similarity).
CC -!- SIMILARITY: Contains 12 fibronectin type I domains.
CC -!- SIMILARITY: Contains 2 fibronectin type II domains.
CC -!- SIMILARITY: Contains 15 fibronectin type III domains.
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or send an email to license@isb-sib.ch).
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EMBL; X08000; AAA30521.2; -.
PIR; A26452; FNBO.
HSSP; P08253; 1KS0.
InterPro; IPR006209; EGF_like.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR003962; FNIII_subd.
PFam; PF00039; fn1; 12.
PFam; PF00040; fn2; 2.
PFam; PF00041; fn3; 15.
DR PRINTS; PR00012; ENTPEBI.
DR PRINTS; PR00013; ENTPEBII.
DR PRINTS; PR00014; ENTPEBII.
DR PRODOM; PD000995; FN_Type_II; 2.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01253; FIBRONECTIN_1; 12.
PROSITE; PS00023; FIBRONECTIN_2; 2.
PROSITE; PS08053; FN3; 15.
KW Acute phase; Alternative splicing; Cell adhesion; Cell shape;
KW Direct protein sequencing; Glycoprotein; Heparin-binding;
KW Phosphorylation; Plasma; Pyrrolidone carboxylic acid; Repeat;
KW Sulfation.
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FT DOMAIN 21 577 Fibrin- and heparin-binding 1.
FT DOMAIN 277 1141 Collagen-binding.
FT DNA_BIND 876 1141 Cell-attachment.
FT DOMAIN 1236 1509 Heparin-binding 2.
FT DOMAIN 1600 1870 Fibrin-binding 2.
FT DOMAIN 1991 2216 Fibronectin type-I 1.
FT DOMAIN 19 59 Fibronectin type-I 2.
FT DOMAIN 64 107 Fibronectin type-I 3.
FT DOMAIN 108 151 Fibronectin type-I 4.
FT DOMAIN 153 197 Fibronectin type-I 5.
FT DOMAIN 198 242 Fibronectin type-I 6.
FT DOMAIN 275 314 Fibronectin type-II 1.
FT DOMAIN 314 373 Fibronectin type-II 2.
FT DOMAIN 374 438 Fibronectin type-I 7.
FT DOMAIN 437 480 Fibronectin type-I 8.
FT DOMAIN 485 527 Fibronectin type-I 9.
FT DOMAIN 528 571 Fibronectin type-III 1.
FT DOMAIN 576 668 Fibronectin type-III 2.
FT DOMAIN 689 778 Fibronectin type-III 3.
FT DOMAIN 780 867 Fibronectin type-III 4.
FT DOMAIN 877 964 Fibronectin type-III 5.
FT DOMAIN 965 1053 Fibronectin type-III 6.
FT DOMAIN 1056 1141 Fibronectin type-III 7.
FT DOMAIN 1142 1234 Fibronectin type-III 8.
FT DOMAIN 1235 1325 Fibronectin type-III 9.
FT DOMAIN 1326 1415 Fibronectin type-III 10.
FT DOMAIN 1416 1505 Fibronectin type-III 11.
FT DOMAIN 1510 1599 Fibronectin type-III 12.
FT DOMAIN 1602 1689 Fibronectin type-III 13.
FT DOMAIN 1692 1780 Fibronectin type-III 14.
FT DOMAIN 1781 1870 Connecting strand 3 (CS-3) (V region).
FT DOMAIN 1871 1990 Fibronectin type-III 15.
FT DOMAIN 1979 2069 Fibronectin type-I 10.
FT DOMAIN 2083 2127 Fibronectin type-I 11.
FT DOMAIN 2128 2170 Fibronectin type-I 12.
FT DOMAIN 2172 2215 Cell attachment site.
FT SITE 1493 1495
FT DISULFID 21 47
FT DISULFID 45 56
FT DISULFID 66 94
FT DISULFID 92 104
FT DISULFID 110 138
FT DISULFID 136 148
FT DISULFID 155 184
FT DISULFID 182 194
FT DISULFID 200 229
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FT DISULFID 277 304
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FT DISULFID 329 355
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FT DISULFID 389 415

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FT DISULFID 403 430
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FT MOD_RES 850 850
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FT CARBOHYD 511 511
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FT CARBOHYD 1944 1944
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Query Match 71.7%; Score 354; DB 1; Length 2265;
Best Local Similarity 74.5%; Pred. No. 1.1e-28;
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Db 1416 VSDVPRDLVIAATPTSLISWDAPAVTVRYRITYGTGSGSPVQEFVTPGSKSTATIS 1475

QY 61 GLKPGVDYITTVAVYDKSDTYKYDDPISINVRT 94
Db 1476 GLKPGVDYITTVAVYAVTGRGDSPASSRPPVSINVRT 1509

RESULT 13
FINC MOUSE
ID_FINC_MOUSE STANDARD; PRT; 2477 AA.
AC F11276; Q61569; Q61569; Q64233; Q80U14;
DT 01-JUL-1989 (Rel. 11, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin precursor (FN).
GN Names=fn1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-920 FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.R., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hate S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villaola D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 1-28 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94131313; PubMed=8299972; DOI=10.1016/0378-1119(93)90036-3;
RA Talls J.F., Weller A., Timpl R., Ekblom M., Ekblom P.;
RT "Regulation of mesenchymal extracellular matrix protein synthesis by
RT transforming growth factor-beta and glucocorticoids in tumor stroma.";
RL J. Cell Sci. 108:2153-2162(1995).
RN [4]
RP SEQUENCE OF 899-2376 FROM N.A.
RA Gorski G., Aros M., Norton P.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 2375-2477 FROM N.A.
RX MEDLINE=88124987; PubMed=3124113;
RA Blatti S.P., Foster D.N., Ranganathan G., Moses H.L., Getz M.J.;
RT "Induction of fibronectin gene transcription and mRNA is a primary
RT response to growth-factor stimulation of AKR-2B cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).
RN [6]
RP SEQUENCE OF 2375-2477 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93011702; PubMed=1327855;
RA Khandjian E.W., Salomon C., Leonard N., Tremblay S., Turler H.;
RT "Fibronectin gene expression in proliferating, quiescent, and SV40-
RT infected mouse kidney cells.";
RL Exp. Cell Res. 202:464-470(1992).
RN [7]
RP STRUCTURE BY NMR OF 1447-1630.
RX MEDLINE=98205278; PubMed=95333887; DOI=10.1006/jmbi.1998.1616;
RA Copie V., Tomita Y., Akiyama S.K., Aota S., Yamada K.M., Venable R.M.,
RA Pastor R.W., Krueger S., Torchia D.A.;
RT "Solution structure and dynamics of linked cell attachment modules of
RT mouse fibronectin containing the RGD and synergy regions: comparison
RL with the human fibronectin crystal structure.";
RN [8]
RP DOWN-REGULATION BY GLUCOCORTICOID.
RX MEDLINE=21600963; PubMed=11737251;
RA Gu Y.-C., Talls J.F., Gullberg D., Timpl R., Ekblom M.;
RT "Glucocorticoids down-regulate the extracellular matrix proteins
RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
RL Eur. J. Haematol. 67:176-184(2001).
CC -!- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC are involved in cell adhesion, cell motility, opsonization, wound
CC healing, and maintenance of cell shape.
CC -!- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
CC variants, connected by 2 disulfide bonds near the carboxyl ends;
CC to a lesser extent homodimers. Interacts with FBLN1 and LGALS3BP
CC (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC ISOID=P11276-1; Sequences=Displayed;
CC -!- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted

```



CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric  
 CC forms), made by fibroblasts, epithelial and other cell types, is  
 CC deposited as fibrils in the extracellular matrix.  
 CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein  
 CC synthesis.  
 CC -!- PTM: Sulfated (By similarity).  
 CC -!- SIMILARITY: Contains 12 fibronectin type I domains.  
 CC -!- SIMILARITY: Contains 2 fibronectin type II domains.  
 CC -!- SIMILARITY: Contains 17 fibronectin type III domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; BC051082; AAH51082.1; -;  
 CC EMBL; Z22729; CAA80422.1; -;  
 CC EMBL; X82402; CAA57796.1; -;  
 CC EMBL; X93167; CAA63654.1; -;  
 CC EMBL; M18194; AAA37636.1; -;  
 CC EMBL; S45680; AAB23491.1; -;  
 CC PIR; A49173; A49173.  
 CC FIR; I48349; I48349.  
 CC PDB; 1MFN; NMR; @=1446-1630.  
 CC PDB; 2MFN; NMR; @=1446-1630.  
 CC MGD; MGI:95566; Fnl.  
 CC GO; GO:0007044; P:cell adhesion; IDA.  
 CC GO; GO:0042060; P:wound healing; IMP.  
 CC InterPro; IPR006209; EGF like.  
 CC InterPro; IPR000083; Fibrinctn1.  
 CC InterPro; IPR003962; FNII subd.  
 CC InterPro; IPR003961; FN III.  
 CC InterPro; IPR008957; FN III-like.  
 CC InterPro; IPR000562; FN\_Type\_II.  
 CC Pfam; PF00039; fn1; 12.  
 CC Pfam; PF00040; fn2; 2.  
 CC Pfam; PF00041; fn3; 17.  
 CC PRINTS; PR00014; FNTYPEIIII.  
 CC ProDom; PD000995; FN\_Type\_II; 2.  
 CC PROSITE; PS00022; EGF\_1; 2.  
 CC PROSITE; PS01253; FIBRONECTIN\_1; 12.  
 CC PROSITE; PS00023; FIBRONECTIN\_2; 2.  
 CC PROSITE; PS00853; FN3; 17.  
 CC 3D-structure; Acute phase; Alternative splicing; Cell adhesion;  
 CC Glycoprotein; Heparin-binding; Phosphorylation; Plasma; Repeat;  
 CC Signal; Sulfation.  
 CC SIGNAL 1 32 By similarity.  
 CC CHAIN 33 2477 Fibronectin.  
 CC DOMAIN 53 273 Fibrin- and heparin-binding 1.  
 CC DOMAIN 308 608 Collagen-binding.  
 CC DNA\_BIND 906 1171  
 CC DOMAIN 1357 1630 Cell-attachment.  
 CC DOMAIN 1811 2081 Heparin-binding 2.  
 CC DOMAIN 2296 2427 Fibrin-binding 2.  
 CC DOMAIN 51 96 Fibronectin type-I 1.  
 CC DOMAIN 96 140 Fibronectin type-I 2.  
 CC DOMAIN 140 185 Fibronectin type-I 3.  
 CC DOMAIN 185 230 Fibronectin type-I 4.  
 CC DOMAIN 230 272 Fibronectin type-I 5.  
 CC DOMAIN 306 343 Fibronectin type-I 6.  
 CC DOMAIN 345 404 Fibronectin type-II 1.  
 CC DOMAIN 405 469 Fibronectin type-II 2.  
 CC DOMAIN 468 516 Fibronectin type-I 7.  
 CC DOMAIN 516 559 Fibronectin type-I 8.  
 CC DOMAIN 559 602 Fibronectin type-I 9.  
 CC DOMAIN 607 699 Fibronectin type-III 1.  
 CC DOMAIN 719 808 Fibronectin type-III 2.  
 CC DOMAIN 810 897 Fibronectin type-III 3.  
 CC DOMAIN 905 994 Fibronectin type-III 4.

FT DOMAIN 995 1083 Fibronectin type-III 5.  
 FT DOMAIN 1091 1171 Fibronectin type-III 6.  
 FT DOMAIN 1172 1264 Fibronectin type-III 7.  
 FT DOMAIN 1265 1355 Fibronectin type-III 8 (extra domain 1).  
 FT DOMAIN 1356 1446 Fibronectin type-III 9.  
 FT DOMAIN 1447 1536 Fibronectin type-III 10.  
 FT DOMAIN 1537 1626 Fibronectin type-III 11.  
 FT DOMAIN 1631 1720 Fibronectin type-III 12.  
 FT DOMAIN 1721 1810 Fibronectin type-III 13 (extra domain 2).  
 FT DOMAIN 1813 1900 Fibronectin type-III 14.  
 FT DOMAIN 1903 1991 Fibronectin type-III 15.  
 FT DOMAIN 1992 2081 Fibronectin type-III 16.  
 FT DOMAIN 2082 2201 Connecting strand 3 (CS-3) (V region).  
 FT DOMAIN 2190 2280 Fibronectin type-III 17.  
 FT DOMAIN 2294 2338 Fibronectin type-I 10.  
 FT DOMAIN 2339 2381 Fibronectin type-I 11.  
 FT DOMAIN 2383 2426 Fibronectin type-I 12.  
 FT SITE 1614 1616 Cell attachment site.  
 FT SITE 2181 2183 Cell attachment site.  
 FT DISULFID 53 79 By similarity.  
 FT DISULFID 77 88 By similarity.  
 FT DISULFID 98 126 By similarity.  
 FT DISULFID 124 136 By similarity.  
 FT DISULFID 142 170 By similarity.  
 FT DISULFID 168 180 By similarity.  
 Query Match 67.4%; Score 333; DB 1; Length 2477;  
 Best Local Similarity 67.0%; Pred. No. 2.3e-26;  
 Matches 63; Conservative 11; Mismatches 20; Indels 0; Gaps 0;  
 Qy 1 VSDVPRDLVVAAPTSLRLISWNRSGLQSRYYRITYGETGNSPVQETVPFWASIIATIS 60  
 Db 1537 VSDIPRDLVIASTPTSLISWEPPAVSVRYRITYGETGNSPVQETVPFGSKSTATIN 1596  
 Qy 61 GLKPGVDYITVYAVTDKSTYKYDDPISINRYT 94  
 Db 1597 NIKPGADYITLYAVTGRGDSPASSKPVSYNYKT 1630  
 RESULT 14  
 FINC\_RAT  
 ID\_FINC\_RAT STANDARD; PRT; 2477 AA.  
 AC P04937; O6LXD9;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Fibronectin precursor (FN).  
 GN Name=Fnl;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Fischer; TISSUE=Liver;  
 RX MEDLINE=88054951; PubMed=2445560;  
 RA Schwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;  
 RT "Multiple sites of alternative splicing of the rat fibronectin gene  
 transcript.";  
 RL EMO J. 6:2573-2580(1987).  
 RN [2]  
 RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.  
 RC STRAIN=Fischer; TISSUE=Liver;  
 RX MEDLINE=88054950; PubMed=3119123;  
 RA Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.;  
 RT "Organization of the fibronectin gene provides evidence for exon  
 shuffling during evolution.";  
 RL EMO J. 6:2565-2572(1987).  
 RN [3]  
 RP SEQUENCE OF 1596-2477 FROM N.A.  
 RX MEDLINE=84082067; PubMed=6317187; DOI=10.1016/0092-8674(83)90175-7;  
 RA Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.;  
 RT "Three different fibronectin mRNAs arise by alternative splicing

RT within the coding region.";

RL Cell 35:421-431(1983).

RN [4]

RX SEQUENCE OF 1722-1810 FROM N.A., AND ALTERNATIVE SPLICING.

RA Oederstatt E., Tamkun J.W., Hynes R.O.;

RT "Repeating modular structure of the fibronectin gene: relationship to

RT protein structure and subunit variation.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:6571-6575(1985).

RN [5]

RX SEQUENCE OF 2052-2237 FROM N.A., AND ALTERNATIVE SPLICING.

RA Tamkun J.W., Schwarzbauer J.E., Hynes R.O.;

RT "A single rat fibronectin gene generates three different mRNAs by

RT alternative splicing of a complex exon.";

RL Proc. Natl. Acad. Sci. U.S.A. 81:5140-5144(1984).

RN [6]

RX SEQUENCE OF 1183-1192; 1385-1399 AND 2287-2300, AND INTERACTION WITH

RA AMBP.

RX PubMed=6089177;

RA Faltenberg C., Enghild J.J., Thøgersen I.B., Salvesen G.,

RT "Isolation and characterization of fibronectin-alpha 1-microglobulin

RT complex in rat plasma.";

RL Biochem. J. 301:745-751(1994).

CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds

CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins

CC are involved in cell adhesion, cell motility, opsonization, wound

CC healing, and maintenance of cell shape.

CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced

CC variants, connected by 2 disulfide bonds near the carboxyl ends;

CC to a lesser extent homodimers. Interacts with FBLN1, AMBP and

CC LGALS3BP (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.

CC -1- ALTERNATIVE PRODUCTS:

CC Comment=Alternative splicing; Named isoforms=4;

CC Event=Each of the "extra domain" and the connecting strand 3

CC are present in some forms of fibronectin and absent in others;

CC Name=1;

CC IsoId=P04937-1; Sequence=Displayed;

CC Name=2; Synonyms=FNIII-13-less;

CC IsoId=P04937-2; Sequence=VSP\_003258;

CC Name=3; Synonyms=Lambda-RLF4-5;

CC IsoId=P04937-3; Sequence=VSP\_003259;

CC Name=4; Synonyms=Lambda-RLF6;

CC IsoId=P04937-4; Sequence=VSP\_003260;

CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted

CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric

CC form), made by fibroblasts, epithelial and other cell types, is

CC deposited as fibrils in the extracellular matrix.

CC -1- PTM: Sulfated (By similarity).

CC -1- SIMILARITY: Contains 12 fibronectin type I domains.

CC -1- SIMILARITY: Contains 2 fibronectin type II domains.

CC -1- SIMILARITY: Contains 17 fibronectin type III domains.

CC -----

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CC -----

DR EMBL; X15906; CAA34020.1; -;

DR EMBL; L29191; AAA41166.1; -;

DR EMBL; L00191; AAA41166.1; JOINED.

DR EMBL; L29191; AAA41167.1; -;

DR EMBL; L00191; AAA41167.1; JOINED.

DR EMBL; L29191; AAA41168.1; -;

DR EMBL; L00191; AAA41168.1; JOINED.

DR EMBL; M11750; AAA41170.1; -;

DR EMBL; X05831; CAA29278.1; -;

DR EMBL; X05832; CAA29279.1; -;

DR EMBL; X05833; CAA29280.1; -;

DR EMBL; X05834; CAA29281.1; -;

DR PIR; S14428; S14428.

DR HSSP; P08253; 1KS0.

DR RGD; 2624; FNI.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR000083; Fibrinctn1.

DR InterPro; IPR003962; FNIII subd.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR008957; FN\_III-like.

DR InterPro; IPR00562; FN\_Type\_II.

DR Pfam; PF00039; fn1; 12.

DR Pfam; PF00040; fn2; 2.

DR Pfam; PF00041; fn3; 17.

DR PRINTS; PR00013; FNTYPEII.

DR PRINTS; PR00014; FNTYPEIII.

DR ProDom; PD000995; FN\_Type\_II; 2.

DR PROSITE; PS00022; EGF 1; 2.

DR PROSITE; PS01253; FIBRONECTIN\_1; 12.

DR PROSITE; PS00023; FIBRONECTIN\_2; 2.

DR PROSITE; PS50853; FN3; 17.

DR Acute phase; Alternative splicing; Cell adhesion;

DR Direct protein sequencing; Glycoprotein; Heparin-binding;

DR Phosphorylation; Plasma; Repeat; Signal; Sulfation.

FT SIGNAL 1 32

FT CHAIN 33 2477 Fibronectin.

FT DOMAIN 53 273 Fibrin- and heparin-binding 1.

FT DOMAIN 308 608 Collagen-binding.

FT DNA\_BIND 906 1171

FT DOMAIN 1357 1630 Cell-attachment.

FT DOMAIN 1811 2081 Heparin-binding 2.

FT DOMAIN 2296 2427 Fibrin-binding 2.

FT DOMAIN 51 91 Fibronectin type-I 1.

FT DOMAIN 96 139 Fibronectin type-I 2.

FT DOMAIN 140 183 Fibronectin type-I 3.

FT DOMAIN 185 229 Fibronectin type-I 4.

FT DOMAIN 230 274 Fibronectin type-I 5.

FT DOMAIN 306 345 Fibronectin type-I 6.

FT DOMAIN 345 404 Fibronectin type-II 1.

FT DOMAIN 405 469 Fibronectin type-II 2.

FT DOMAIN 468 511 Fibronectin type-I 7.

FT DOMAIN 516 558 Fibronectin type-I 8.

FT DOMAIN 559 602 Fibronectin type-I 9.

FT DOMAIN 607 699 Fibronectin type-III 1.

FT DOMAIN 719 808 Fibronectin type-III 2.

FT DOMAIN 810 897 Fibronectin type-III 3.

FT DOMAIN 907 994 Fibronectin type-III 4.

FT DOMAIN 995 1083 Fibronectin type-III 5.

FT DOMAIN 1091 1171 Fibronectin type-III 6.

FT DOMAIN 1172 1264 Fibronectin type-III 7.

FT DOMAIN 1265 1355 Fibronectin type-III 8 (extra domain 1).

FT DOMAIN 1356 1446 Fibronectin type-III 9.

FT DOMAIN 1447 1536 Fibronectin type-III 10.

FT DOMAIN 1537 1626 Fibronectin type-III 11.

FT DOMAIN 1631 1720 Fibronectin type-III 12.

FT DOMAIN 1721 1810 Fibronectin type-III 13 (extra domain 2).

FT DOMAIN 1813 1900 Fibronectin type-III 14.

FT DOMAIN 1903 1991 Fibronectin type-III 15.

FT DOMAIN 1992 2081 Fibronectin type-III 16.

FT DOMAIN 2082 2201 Connecting strand 3 (CS-3) (V region).

FT DOMAIN 2190 2280 Fibronectin type-III 17.

FT DOMAIN 2284 2338 Fibronectin type-I 10.

FT DOMAIN 2339 2381 Fibronectin type-I 11.

FT DOMAIN 2383 2426 Fibronectin type-I 12.

FT SITE 1614 1616 Cell attachment site.

FT SITE 2181 2183 Cell attachment site.

FT SITE 53 79 By similarity.

FT DISULFID 77 88 By similarity.

FT DISULFID 98 126 By similarity.

FT DISULFID 124 136 By similarity.

FT DISULFID 142 170 By similarity.

FT DISULFID 168 180 By similarity.

FT DISULFID 187 216 By similarity.

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FT DISULFID 214 226 By similarity.
FT DISULFID 232 261 By similarity.
FT DISULFID 259 271 By similarity.
FT DISULFID 308 335 By similarity.
FT DISULFID 333 342 By similarity.
FT DISULFID 360 386 By similarity.
FT DISULFID 374 401 By similarity.
FT DISULFID 420 446 By similarity.
FT DISULFID 434 461 By similarity.
FT DISULFID 470 498 By similarity.
FT DISULFID 496 508 By similarity.
FT DISULFID 518 545 By similarity.
FT DISULFID 543 555 By similarity.
FT DISULFID 561 589 By similarity.
FT DISULFID 587 599 By similarity.
FT DISULFID 2296 2325 By similarity.
FT DISULFID 2323 2335 By similarity.
FT DISULFID 2341 2368 By similarity.
FT DISULFID 2366 2378 By similarity.
FT DISULFID 2385 2409 By similarity.
FT DISULFID 2407 2423 By similarity.
FT DISULFID 2458 Interchain (with C-2462).

Query Match 67.4%; Score 333; DB 1; Length 2477;
Best Local Similarity 68.1%; Pred. NO. 2.3e-26;
Matches 64; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 VSDPRDELVAAPTSLISNRSLGLOSRYRYTYGTGGSPVOEFTVPWASIAIIS 60
Db 1537 VSDPRDELVAAPTSLISNRSLGLOSRYRYTYGTGGSPVOEFTVPWASIAIIS 1596

Qy 61 GLKPGVDYITVYAVTKSDTYKYDDPISINRYT 94
Db 1597 NIKPGADYITVYAVTGRGDSPPASSKPVSYNYQT 1630

RESULT 15
ID_FINC CHICK STANDARD; PRT; 1256 AA.
AC P11722; Q90921;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibronectin (FN) (Fragments).
GN Name=FNI;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE OF 1-50 FROM N.A.
RX MEDLINE=83117850; PubMed=6572007;
RA Hirano H., Yamada Y., Sullivan M., de Crombrughe B., Pastan I.,
RA Yamada K.M.;
RT "Isolation of genomic DNA clones spanning the entire fibronectin
RT gene."
RL Proc. Natl. Acad. Sci. U.S.A. 80:46-50(1983).
RN [2]
RP SEQUENCE OF 51-1256 FROM N.A.
RC STRAIN=white leghorn;
RA Norton P.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 227-415 FROM N.A.
RX MEDLINE=96183658; PubMed=8603103; DOI=10.1016/0167-4889(95)00183-2;
RA Gehris A.L., Brandli D.W., Lewis S.D., Bennett V.D.;
RT "The exon encoding the fibronectin type III-9 repeat is constitutively
RT included in the mRNA from chick limb mesenchyme and cartilage."
RL Biochim. Biophys. Acta 1311:5-12(1996).
RN [4]
RP SEQUENCE OF 327-599 FROM N.A.
RX MEDLINE=88050950; PubMed=2823899; DOI=10.1016/0167-4781(87)90070-4;

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RA Kubomura S., Obara M., Karasaki Y., Taniguchi H., Gotoh S., Tsuda T.,
RA Higashi K., Ohsato K., Hiarno H.;
RT "Genetic analysis of the cell binding domain region of the chicken
RL fibronectin gene."
RN Biochim. Biophys. Acta 910:171-181(1987).
RP [5]
RX SEQUENCE OF 413-1256 FROM N.A.
RA MEDLINE=88142820; PubMed=2830487;
RT Norton P.A., Hynes R.O.;
RL "Alternative splicing of chicken fibronectin in embryos and in normal
RP and transformed cells."
RN Mol. Cell. Biol. 7:4297-4307(1987).
CC -|- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC are involved in cell adhesion, cell motility, opsonization, wound
CC healing, and maintenance of cell shape.
CC -|- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
CC variants, connected by 2 disulfide bonds near the carboxyl ends;
CC to a lesser extent homodimers.
CC -|- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC IsoId=P11722-1; Sequence=Displayed;
CC -|- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
CC forms), made by fibroblasts, epithelial and other cell types, is
CC deposited as fibrils in the extracellular matrix.
CC -|- PTM: Sulfated (By similarity).
CC -|- SIMILARITY: Contains at least 2 fibronectin type I domains.
CC -|- SIMILARITY: Contains at least 11 fibronectin type III domains.
CC -----
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CC -----
DR EMBL; V00432; CAA23714.1; -
DR EMBL; U21327; AAA73566.1; -
DR EMBL; X06533; CAA29781.1; -
DR EMBL; M26186; AAA48772.1; ALT_SEQ.
DR EMBL; U20386; AAB01062.1; -
DR PIR; A28512; A28512.
DR PIR; A29355; A29355.
DR PIR; S71465; S71465.
DR HSSP; P02751; 1FNH.
DR InterPro; IPR000083; Fibnctnl.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR003962; FNIII_subd.
DR PRINTS; PR00012; ENTPEI.
DR PRINTS; PR00014; FNTYPEIII.
DR PROSITE; PS01253; FIBRONECTIN_1; 2.
DR PROSITE; PS00023; FIBRONECTIN_2; PARTIAL.
DR PROSITE; PS00853; FN3; 11.
KW Acute phase; Alternative splicing; Cell adhesion; Glycoprotein;
KW Heparin-binding; Plasma; Repeat; Sulfation.
FT NON_TER 1
FT NON_CONS 50 51 Fibronectin type-III 1.
FT DOMAIN 51 143 Fibronectin type-III 2.
FT DOMAIN 144 234 Fibronectin type-III 3.
FT DOMAIN 235 325 Cell-attachment.
FT DOMAIN 236 509 Heparin-binding 2.
FT DOMAIN 690 961 Fibrin-binding 2 (By similarity).
FT DOMAIN 1153 1226 Fibronectin type-III 4.
FT DOMAIN 326 415 Fibronectin type-III 5.
FT DOMAIN 416 505

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FT	DOMAIN	510	599	Fibronectin type-III 6 (extra domain 1).
FT	DOMAIN	600	689	Fibronectin type-III 7 (extra domain 2).
FT	DOMAIN	692	779	Fibronectin type-III 8.
FT	DOMAIN	782	871	Fibronectin type-III.
FT	DOMAIN	872	961	Fibronectin type-III.
FT	DOMAIN	962	1082	Connecting strand 3 (CS-3) (V region).
FT	DOMAIN	1071	1160	Fibronectin type-III 11.
FT	DOMAIN	1174	1218	Fibronectin type-I.
FT	DOMAIN	1219	>1256	Fibronectin type-I.
FT	SITE	493	495	Cell attachment site.
FT	DISULFID	1176	1205	By similarity.
FT	DISULFID	1203	1215	By similarity.
FT	DISULFID	1221	1248	By similarity.
FT	CARBOHYD	122	122	N-linked (GlcNac. . .) (By similarity).
FT	CARBOHYD	1078	1078	N-linked (GlcNac. . .) (By similarity).
FT	CARBOHYD	1034	1034	O-linked (GalNac. . .) (By similarity).
FT	CARBOHYD	1035	1035	O-linked (GalNac. . .) (By similarity).
FT	CONFLICT	516	516	Q -> P (in Ref. 4).
FT	CONFLICT	569	572	EGFQ -> QGLE (in Ref. 4).
FT	NON_TER	1256	1256	
SQ	SEQUENCE	1256 AA;	137435 MW;	345A4CA0E4D71D9B CRC64;
Query Match 63.0%; Score 311; DB 1; Length 1256;				
Best Local Similarity 64.9%; Pred. No. 2.4e-24;				
Matches 61; Conservative 11; Mismatches 22; Indels 0; Gaps 0;				
QY	1	VSDVPRDLEVAATPTSRLLSNRSLQSRYYRITYGETGNSPVOEFTVPPWASTATIS	60	
Db	416	VSDVPRDLEVNPTSPTSLSLEISWDAPAVTVYRITYGETGSGSPVOEFTVPGTMSRATIT	475	
QY	61	GLKPGVDYTIITVYAVTDKSDTYKYDDPISINVRT	94	
Db	476	GLKPGVDYTIITVYAVTGRGDSPASSKPVTVYKTV	509	

Search completed: May 18, 2005, 15:34:55  
Job time : 181 secs